

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Choi et. al.
- (ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
- (iii) NUMBER OF SEQUENCES: 452
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Human Genome Sciences, Inc.
  - (B) STREET: 9410 Key West Avenue
  - (C) CITY: Rockville
  - (D) STATE: Maryland
  - (E) COUNTRY: USA
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
  - (B) COMPUTER: HP Vectra 486/33
  - (C) OPERATING SYSTEM: MSDOS version 6.2
  - (D) SOFTWARE: ASCII Text
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: Unassigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/961,083
  - (B) FILING DATE: OCT-30-1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Michelle S. Marks
  - (B) REGISTRATION NUMBER: 41,971
  - (C) REFERENCE/DOCKET NUMBER: PB340P2C1
- (vi) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (301) 309-8504
  - (B) TELEFAX: (301) 309-8512

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

----(xi)-SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCCTGAAC GCCGCGTCAA	60
TGCCCCAAGCT AATGATATTC CCACAGATTT GGTTAAGGCA ATCGTTTCTA TCGAAGACCA	120
TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA	180
TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC	240
TTACTTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT	300
AGCGATTTCAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA	360
GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA	420
AGACCTCAAT AATTTAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC	480
AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT	540
ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC	600
ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA	660
TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC	720
AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT	780
TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT	840
TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA	900
TGTTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA	960
ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT	1020
CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG	1080
GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC	1140
CGTGGAAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG	1200
AATCGACTAC CCAAGTATTC ACTACTCAA TGCCATTTCA AGTAACACAA CCGAATCAGA	1260
CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAAATGG	1320
TGGAACCTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA	1380
AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA	1440
CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC	1500
TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA	1560
GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT	1620
GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT	1680
CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA	1740

0075271 042200

TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG 1800  
 TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC 1860  
 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCACCTCCA AGCACAAATA ATAGTACGAC 1920  
 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980  
 TCCTCAACCA GCACAACCA 1999

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu  
 1 5 10 15  
 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys  
 20 25 30  
 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile  
 35 40 45  
 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn  
 50 55 60  
 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr  
 65 70 75 80  
 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln  
 85 90 95  
 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu  
 100 105 110  
 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr  
 115 120 125  
 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn  
 130 135 140  
 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro  
 145 150 155 160  
 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg  
 165 170 175  
 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu  
 180 185 190  
 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser  
 195 200 205  
 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys

210				215				220							
Glu 225	Val	Ile	Asn	Gln 230	Val	Glu	Glu	Glu	Thr	Gly 235	Tyr	Asn	Leu	Leu	Thr 240
Thr	Gly	Met	Asp	Val 245	Tyr	Thr	Asn	Val	Asp 250	Gln	Glu	Ala	Gln	Lys	His 255
Leu	Trp	Asp	Ile 260	Tyr	Asn	Thr	Asp	Glu 265	Tyr	Val	Ala	Tyr	Pro	Asp	Asp 270
Glu	Leu	Gln 275	Val	Ala	Ser	Thr	Ile 280	Val	Asp	Val	Ser	Asn 285	Gly	Lys	Val
Ile	Ala 290	Gln	Leu	Gly	Ala	Arg 295	His	Gln	Ser	Ser	Asn 300	Val	Ser	Phe	Gly
Ile 305	Asn	Gln	Ala	Val	Glu 310	Thr	Asn	Arg	Asp	Trp 315	Gly	Ser	Thr	Met	Lys 320
Pro	Ile	Thr	Asp	Tyr 325	Ala	Pro	Ala	Leu	Glu 330	Tyr	Gly	Val	Tyr	Asp	Ser 335
Thr	Ala	Thr	Ile 340	Val	His	Asp	Glu	Pro 345	Tyr	Asn	Tyr	Pro	Gly 350	Thr	Asn
Thr	Pro	Val	Tyr 355	Asn	Trp	Asp	Arg	Gly 360	Tyr	Phe	Gly	Asn 365	Ile	Thr	Leu
Gln	Tyr	Ala	Leu	Gln	Gln	Ser 375	Arg	Asn	Val	Pro	Ala	Val 380	Glu	Thr	Leu
Asn 385	Lys	Val	Gly	Leu	Asn 390	Arg	Ala	Lys	Thr	Phe 395	Leu	Asn	Gly	Leu	Gly 400
Ile	Asp	Tyr	Pro	Ser 405	Ile	His	Tyr	Ser	Asn 410	Ala	Ile	Ser	Ser	Asn	Thr 415
Thr	Glu	Ser	Asp 420	Lys	Lys	Tyr	Gly	Ala 425	Ser	Ser	Glu	Lys	Met 430	Ala	Ala
Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Gly 440	Gly	Thr	Tyr	Tyr	Lys 445	Pro	Met	Tyr
Ile	His 450	Lys	Val	Val	Phe	Ser 455	Asp	Gly	Ser	Glu	Lys 460	Glu	Phe	Ser	Asn
Val 465	Gly	Thr	Arg	Ala	Met 470	Lys	Glu	Thr	Thr	Ala 475	Tyr	Met	Met	Thr	Asp 480
Met	Met	Lys	Thr	Val 485	Leu	Thr	Tyr	Gly	Thr 490	Gly	Arg	Asn	Ala	Tyr	Leu 495
Ala	Trp	Leu	Pro 500	Gln	Ala	Gly	Lys	Thr 505	Gly	Thr	Ser	Asn	Tyr 510	Thr	Asp
Glu	Glu	Ile	Glu	Asn	His	Ile	Lys 520	Thr	Ser	Gln	Phe	Val 525	Ala	Pro	Asp
Glu	Leu	Phe	Ala	Gly	Tyr	Thr	Arg 535	Lys	Tyr	Ser	Met 540	Ala	Val	Trp	Thr
Gly	Tyr	Ser	Asn	Arg	Leu	Thr	Pro	Leu	Val	Gly	Asn	Gly	Leu	Thr	Val



(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 1714 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AAATTACAAT	ACGGACTATG	AATTGACCTC	TGGAGAAAAA	TTACCTCTTC	CTAAAGAGAT	60
TTCAGGTTAC	ACTTATATTG	GATATATCAA	AGAGGGAAAA	ACGACTTCTG	AGTCTGAAGT	120
AAGTAATCAA	AAGAGTTCAG	TTGCCACTCC	TACAAAACAA	CAAAAGGTGG	ATTATAATGT	180
TACACCGAAT	TTTGTAGACC	ATCCATCAAC	AGTACAAGCT	ATTCAGGAAC	AAACACCTGT	240
TTCTTCAACT	AAGCCGACAG	AAGTTCAAGT	AGTTGAAAAA	CCTTTCTCTA	CTGAATTAAT	300
CAATCCAAGA	AAAGAAGAGA	AACAATCTTC	AGATTCTCAA	GAACAATTAG	CCGAACATAA	360
GAATCTAGAA	ACGAAGAAAG	AGGAGAAGAT	TTCTCCAAAA	GAAAAGACTG	GGGTAAATAC	420
ATTAAATCCA	CAGGATGAAG	TTTTATCAGG	TCAATTGAAC	AAACCTGAAC	TCTTATATCG	480
TGAGGAAACT	ATGGAGACAA	AAATAGATTT	TCAAGAAGAA	ATTCAAGAAA	ATCCTGATTT	540
AGCTGAAGGA	ACTGTAAGAG	TAAACAAGA	AGGTAAATTA	GGTAAGAAAG	TTGAAATCGT	600
CAGAATATTC	TCTGTAAACA	AGGAAGAAGT	TTCGCGAGAA	ATTGTTTCAA	CTTCAACGAC	660
TGCGCCTAGT	CCAAGAATAG	TCGAAAAAGG	TACTAAAAAA	ACTCAAGTTA	TAAAGGAACA	720
ACCTGAGACT	GGTGTAGAAC	ATAAGGACGT	ACAGTCTGGA	GCTATTGTTG	AACCCGCAAT	780
TCAGCCTGAG	TTGCCCGAAG	CTGTAGTAAG	TGACAAAGGC	GAACCAGAAG	TTCAACCTAC	840

ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA 900  
TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG 960  
TAATATTGAG CAAGTAAAC CTGAAACTCC GGTGAGAAG ACCAAAGAAC AAGGTCCAGA 1020  
AAAAACTGAA GAAGTTCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG 1080  
TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC 1140  
AACAACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGAAGTGTC 1200  
CAGTAATCCT AGTGATTGCA CAACCTCAGT TGGAGAATCA AATAAACCAG AACATAATGA 1260  
CTCTAAAAAT GAAAATTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG 1320  
CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC 1380  
ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG 1440  
TGATTCAAAA CCACCAAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA 1500  
ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA 1560  
CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA 1620  
AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC 1680  
ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA 1714

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu  
1 5 10 15  
Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly  
20 25 30  
Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala  
35 40 45  
Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe  
50 55 60  
Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val  
65 70 75 80  
Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser  
85 90 95  
Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser  
100 105 110



Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser  
 450 455 460  
 Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser  
 465 470 475 480  
 Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly  
 485 490 495  
 Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly  
 500 505 510  
 Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser  
 515 520 525  
 Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln  
 530 535 540  
 Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr  
 545 550 555 560  
 Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu  
 565 570

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTCAAAAG ACAATCGTCC TTGCTACAGC	60
TGGCGACGTG CCACCATTG ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA	120
AGTTTTAAAG GCAGTAGATG AAAAAGCTCAG CGACTACGAG ATTCAATTCC AAAGAACCGC	180
CTGGGAGAGC ATCTTCCAG GACTTGATTG TGGTCACTAT CAGGCTGCGG CCAATAACTT	240
GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC	300
CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA	360
AACAACACAA GAGGATACCG GAACTTCTAA CGCTCAATTC ATCAATAACT GGAATCAGAA	420
ACACACTGAT AATCCCGCTA CAATTAATTT TTCTGGTGAG GATATTGGTA AACGAATCCT	480
AGACCTTGCT AACGGAGAGT TTGATTTCTT AGTTTTTGAC AAGGTATCCG TTCAAAAGAT	540
TATCAAGGAC CGTGGTTTAG ACCTCTCAGT CGTTGATTTA CCTTCTGCAG ATAGCCCCAG	600
CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTTAAA GAGCAATTTG ATAAAGCGCT	660
CAAAGAACTC TATCAAGACG GAACCCTTGA AAAACTCAGC AATACCTATC TAGGTGGTTC	720
TTACCTCCCA GATCAATCTC AGTTACAA	748

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val  
 1 5 10 15  
 Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly  
 20 25 30  
 Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys  
 35 40 45  
 Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile  
 50 55 60  
 Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn Leu  
 65 70 75 80  
 Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile  
 85 90 95  
 Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr  
 100 105 110  
 Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr  
 115 120 125  
 Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn  
 130 135 140  
 Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu  
 145 150 155 160  
 Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser  
 165 170 175  
 Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp  
 180 185 190  
 Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp  
 195 200 205  
 Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr  
 210 215 220  
 Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser  
 225 230 235 240  
 Tyr Leu Pro Asp Gln Ser Gln Leu Gln  
 245

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT 60  
 CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGAAGGTTT 120  
 GCAGGCTTGG GGTAAGAAGC ACAATCTTTC AAAAGATAAC GGTTTCACTT ACTTCCAATC 180  
 AACAAAGTGAA GCTGACTACG CTAACAACCTT GCAACAAGCG GCTGGAAGTT ACAACCTAAT 240  
 CTTCGGTGTT GGTTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAG AACACACTGA 300  
 CTTGAACTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC 360  
 TTTCGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC 420  
 AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG 480  
 ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG 540  
 TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC 600  
 AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC 660  
 TCTCAACGAA AGCCGTCCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA 720  
 AGAAGCAGAA GGTAATACA CTTCTAAAGA TGGCAAAGAA TCAAACTTTG TTCTTGATC 780  
 TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAGGCAG AAAGAGGAGA 840  
 ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTTG ACTTGGCAGT 900  
 AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCGAAGAT GCAAAAGCTA AAATCCTTGA 960  
 TGAAGCGTA AAAGTTCCTG AAAAA 985

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr  
 1 5 10 15

Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe  
 20 25 30

Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn

35 40 45  
 Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala  
 50 55 60  
 Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile  
 65 70 75 80  
 Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys  
 85 90 95  
 Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp  
 100 105 110  
 Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr  
 115 120 125  
 Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly  
 130 135 140  
 Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly  
 145 150 155 160  
 Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val  
 165 170 175  
 Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala  
 180 185 190  
 Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly  
 195 200 205  
 Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser  
 210 215 220  
 Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln  
 225 230 235 240  
 Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe  
 245 250 255  
 Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile  
 260 265 270  
 Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val  
 275 280 285  
 Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser  
 290 295 300  
 Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp  
 305 310 315 320  
 Gly Ser Val Lys Val Pro Glu Lys  
 325

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC 60  
 AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGGATG AATTGTTAGC AAATGCCAAC 120  
 AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGTGAC 180  
 TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAA ACTATGATAT TGCCTTTGCA 240  
 GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA 300  
 AAAGAAGGTA AAGACCTTTA CAAAGCACTT GACCCAGCTT ACATCAAGGG TAATACTGTA 360  
 AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAACCTTGCC 420  
 TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA 480  
 ACTCTTGAGC CAGTCTTGAA ACAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT 540  
 ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA 600  
 TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT 660  
 TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC 720  
 GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA 780  
 ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTTAC GTGTTGCCAA CAAAGATATC 840  
 CAAATCAAAC CAATTACTAA CTTTCATCAAG NAAAACCAAA CAACACAAGT TGCTAACTTT 900  
 GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT 960  
 ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA 1020  
 ATTGAAGGTA AAGAAAACCG TGTTGCGGTT CTTGATGGCT ACAAAGGAAA CACTCACATG 1080  
 GGTGGATGGA ACACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA 1140  
 CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT 1200  
 ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA 1260  
 TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG 1320  
 GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC 1380  
 GATGAATTCT TGAAAAACAA AAAA 1404

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Gly Asn Leu Thr Gly Asn Ser Lys Lys Ala Ala Asp Ser Gly Asp  
 1 5 10 15  
 Lys Pro Val Ile Lys Met Tyr Gln Ile Gly Asp Lys Pro Asp Asn Leu  
 20 25 30  
 Asp Glu Leu Leu Ala Asn Ala Asn Lys Ile Ile Glu Glu Lys Val Gly  
 35 40 45  
 Ala Lys Leu Asp Ile Gln Tyr Leu Gly Trp Gly Asp Tyr Gly Lys Lys  
 50 55 60  
 Met Ser Val Ile Thr Ser Ser Gly Glu Asn Tyr Asp Ile Ala Phe Ala  
 65 70 75 80  
 Asp Asn Tyr Ile Val Asn Ala Gln Lys Gly Ala Tyr Ala Asp Leu Thr  
 85 90 95  
 Glu Leu Tyr Lys Lys Glu Gly Lys Asp Leu Tyr Lys Ala Leu Asp Pro  
 100 105 110  
 Ala Tyr Ile Lys Gly Asn Thr Val Asn Gly Lys Ile Tyr Ala Val Pro  
 115 120 125  
 Val Ala Ala Asn Val Ala Ser Ser Gln Asn Phe Ala Phe Asn Gly Thr  
 130 135 140  
 Leu Leu Ala Lys Tyr Gly Ile Asp Ile Ser Gly Val Thr Ser Tyr Glu  
 145 150 155 160  
 Thr Leu Glu Pro Val Leu Lys Gln Ile Lys Glu Lys Ala Pro Asp Val  
 165 170 175  
 Val Pro Phe Ala Ile Gly Lys Val Phe Ile Pro Ser Asp Asn Phe Asp  
 180 185 190  
 Tyr Pro Val Ala Asn Gly Leu Pro Phe Val Ile Asp Leu Glu Gly Asp  
 195 200 205  
 Thr Thr Lys Val Val Asn Arg Tyr Glu Val Pro Arg Phe Lys Glu His  
 210 215 220  
 Leu Lys Thr Leu His Lys Phe Tyr Glu Ala Gly Tyr Ile Pro Lys Asp  
 225 230 235 240  
 Val Ala Thr Ser Asp Thr Ser Phe Asp Leu Gln Gln Asp Thr Trp Phe  
 245 250 255  
 Val Arg Glu Glu Thr Val Gly Pro Ala Asp Tyr Gly Asn Ser Leu Leu  
 260 265 270  
 Ser Arg Val Ala Asn Lys Asp Ile Gln Ile Lys Pro Ile Thr Asn Phe  
 275 280 285  
 Ile Lys Xaa Asn Gln Thr Thr Gln Val Ala Asn Phe Val Ile Ser Asn  
 290 295 300  
 Asn Ser Lys Asn Lys Glu Lys Ser Met Glu Ile Leu Asn Leu Leu Asn  
 305 310 315 320  
 Thr Asn Pro Glu Leu Leu Asn Gly Leu Val Tyr Gly Pro Glu Gly Lys

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325	330	335
Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp		
340	345	350
Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn		
355	360	365
Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn		
370	375	380
Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe		
385	390	400
Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn		
405	410	415
Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro		
420	425	430
Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala		
435	440	445
Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu		
450	455	460
Lys Asn Lys Lys		
465		

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTG GTTATC AACGGAAGG CACCATTTC AGTGTATTC CAAGACTACA TGGCTAAGAA	240
ATTGGAAAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTG GTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAACTTGC TATGTTGAAA ACCTTG GTTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAA ACTCAA TCACACCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780  
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840  
 CGCAGCTCGC TGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900  
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys	1	5	10	15
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu	20	25	30	
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val	35	40	45	
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn	50	55	60	
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys	65	70	75	80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His	85	90	95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro	100	105	110	
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu	115	120	125	
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu	130	135	140	
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile	145	150	155	160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly	165	170	175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys	180	185	190	
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn	195	200	205	
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln	210	215	220	

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Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala  
225 230 235 240

Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp  
245 250 255

Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp  
260 265 270

Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr  
275 280 285

Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys  
290 295 300

Gly Phe Thr Asn Glu Phe Val Lys  
305 310

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT	60
CGATGAAATC AAAAAAGCG GTGAACTGCG AATCGCCGTG TTTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTAA ATACATTTCA GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTGCTATC	360
ACCTAAGACT GGTCTCATT CAGACGTCAA ACAACTTGAA GGTAAACCT TAATTGTCAC	420
AAAAGGA 3 ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTGACT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC	540
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAT AAAGGATTTG AAGTAGGAAT	600
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAAACTTCT TCCACAAGGC	720
CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 amino acids  
 (B) TYPE: amino acid

0955274 042204  
 102210 1259260

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Ser	Gly	Gly	Asn	Ala	Gly	Ser	Ser	Ser	Gly	Lys	Thr	Thr	Ala	Lys	1	5	10	15
Ala	Arg	Thr	Ile	Asp	Glu	Ile	Lys	Lys	Ser	Gly	Glu	Leu	Arg	Ile	Ala	20	25	30	
Val	Phe	Gly	Asp	Lys	Lys	Pro	Phe	Gly	Tyr	Val	Asp	Asn	Asp	Gly	Ser	35	40	45	
Thr	Lys	Val	Arg	Tyr	Asp	Ile	Glu	Leu	Gly	Asn	Gln	Leu	Ala	Gln	Asp	50	55	60	
Leu	Gly	Val	Lys	Val	Lys	Tyr	Ile	Ser	Val	Asp	Ala	Ala	Asn	Arg	Ala	65	70	75	80
Glu	Tyr	Leu	Ile	Ser	Asn	Lys	Val	Asp	Ile	Thr	Leu	Ala	Asn	Phe	Thr	85	90	95	
Val	Thr	Asp	Glu	Arg	Lys	Lys	Gln	Val	Asp	Phe	Ala	Leu	Pro	Tyr	Met	100	105	110	
Lys	Val	Ser	Leu	Gly	Val	Val	Ser	Pro	Lys	Thr	Gly	Leu	Ile	Thr	Asp	115	120	125	
Val	Lys	Gln	Leu	Glu	Gly	Lys	Thr	Leu	Ile	Val	Thr	Lys	Gly	Thr	Thr	130	135	140	
Ala	Glu	Thr	Tyr	Phe	Glu	Lys	Asn	His	Pro	Glu	Ile	Lys	Leu	Gln	Lys	145	150	155	160
Tyr	Asp	Gln	Tyr	Ser	Asp	Ser	Tyr	Gln	Ala	Leu	Leu	Asp	Gly	Arg	Gly	165	170	175	
Asp	Ala	Phe	Ser	Thr	Asp	Asn	Thr	Glu	Val	Leu	Ala	Trp	Ala	Leu	Glu	180	185	190	
Asn	Lys	Gly	Phe	Glu	Val	Gly	Ile	Thr	Ser	Leu	Gly	Asp	Pro	Asp	Thr	195	200	205	
Ile	Ala	Ala	Ala	Val	Gln	Lys	Gly	Asn	Gln	Glu	Leu	Leu	Asp	Phe	Ile	210	215	220	
Asn	Lys	Asp	Ile	Glu	Lys	Leu	Gly	Lys	Glu	Asn	Phe	Phe	His	Lys	Ala	225	230	235	240
Tyr	Glu	Lys	Thr	Leu	His	Pro	Thr	Tyr	Gly	Asp	Ala	Ala	Lys	Ala	Asp	245	250	255	
Asp	Leu	Val	Val	Glu	Gly	Gly	Lys	Val	Asp	260	265								

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCA	ACTAT	GGTAA	ATCTG	CGGAT	GGCAC	AGTGAC	CATC	GAGTAT	TTTCA	ACCAG	AAAAA	60
AGAAAT	GACC	AAAAC	CTTGG	AAGAA	ATCAC	TCGTGA	TTTT	GAGAAG	GAAA	ACCCT	AAGAT	120
CAAGGT	CAAA	GTCGT	CAATG	TACCA	AATGC	TGGTGA	AGTA	TTGAAG	ACAC	GCGTT	CTCGC	180
AGGAGAT	GTG	CCTGAT	GTGG	TCAAT	ATTTA	CCCAC	AGTCC	ATCGAA	CTGC	AAGAAT	GGGC	240
AAAAGC	AGGT	GTTTTT	GAAAG	ATTTG	AGCAA	CAAAGA	CTAC	CTGAA	ACGCG	TGAAAA	ATGG	300
CTACGCT	GAA	AAATAT	GCTG	TAAAC	GAAAA	AGTTT	TACAAC	GTTCT	TTTTTA	CAGCT	AATGC	360
TTATGGA	ATT	TACTACA	ACA	AAGATA	AAATT	CGAAGA	ACTG	GGCTT	GAAAG	TTCTT	GAAAC	420
CTGGGAT	GAA	TTTGA	ACAGT	TAGTCA	AAGA	TATCGT	TGCT	AAAGG	ACAAA	CACCAT	TTGG	480
AATTGC	AGGT	GCAGAT	GCTT	GGACAC	TCAA	TGGTT	TACAAT	CAATT	AGCCT	TTGCG	ACAGC	540
AACAGG	TGGA	GGAAA	AGAAG	CAAAT	CAATA	CCTTC	GTTAT	TCTCA	ACCAA	ATGCC	ATTAA	600
ATTGTC	GGAT	CCGATT	TATGA	AAGAT	GATAT	CAAGGT	CATG	GACAT	CCTTC	GCATCA	ATGG	660
ATCTA	AGCAA	AAGAAC	TGGG	AAGGT	GCTGG	CTATA	CCGAT	GTTAT	CGGAG	CCTTC	GCACG	720
TGGGGAT	GTG	CTCAT	GACAC	CAAAT	GGGTC	TTGGG	CGATC	ACAGC	GATTA	ATGAAC	AAAAA	780
ACCGAAC	TTT	AAGATT	TGGGA	CCTTC	CATGAT	TCCAGG	AAAAA	GAAAA	AGGAC	AAAGCT	TAAAC	840
CGTTGGT	GCG	GGAGAC	TTGG	CATGGT	CTAT	CTCAGC	CACC	ACCAA	ACATC	CAAAAG	AAGC	900
CAATGC	CCTTT	GTGGA	ATATA	TGACCC	GTCC	AGAAGT	CATG	CAAAA	ATACT	ACGATG	TGGA	960
CGGATCT	CCA	ACAGC	GATCG	AAGGGG	TCAA	ACAAGC	AGGA	GAAGAT	TCAC	CGCTT	GCTGG	1020
TATGACC	GAA	TATGC	CTTTA	CGGAT	CGTCA	CTTGGT	CTGG	TTGCA	ACAAT	ACTGG	ACCAG	1080
TGAAGC	AGAC	TTCCAT	ACCT	TGACCAT	GAA	CTATGT	CTTG	ACCGGT	GATA	AACAAG	GCGAT	1140
GGTCAAT	GAT	TTGAAT	GCCT	TCTTTA	ACCC	GATGAA	AGCG	GATGT	GCGAT			1189

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5				10					15		

Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp  
 20 25 30  
 Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro  
 35 40 45  
 Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro  
 50 55 60  
 Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala  
 65 70 75 80  
 Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg  
 85 90 95  
 Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr  
 100 105 110  
 Asn Val Pro Phe Thr Ala Asn Ala Tyr Gly Ile Tyr Tyr Asn Lys Asp  
 115 120 125  
 Lys Phe Glu Glu Leu Gly Leu Lys Val Pro Glu Thr Trp Asp Glu Phe  
 130 135 140  
 Glu Gln Leu Val Lys Asp Ile Val Ala Lys Gly Gln Thr Pro Phe Gly  
 145 150 155 160  
 Ile Ala Gly Ala Asp Ala Trp Thr Leu Asn Gly Tyr Asn Gln Leu Ala  
 165 170 175  
 Phe Ala Thr Ala Thr Gly Gly Gly Lys Glu Ala Asn Gln Tyr Leu Arg  
 180 185 190  
 Tyr Ser Gln Pro Asn Ala Ile Lys Leu Ser Asp Pro Ile Met Lys Asp  
 195 200 205  
 Asp Ile Lys Val Met Asp Ile Leu Arg Ile Asn Gly Ser Lys Gln Lys  
 210 215 220  
 Asn Trp Glu Gly Ala Gly Tyr Thr Asp Val Ile Gly Ala Phe Ala Arg  
 225 230 235 240  
 Gly Asp Val Leu Met Thr Pro Asn Gly Ser Trp Ala Ile Thr Ala Ile  
 245 250 255  
 Asn Glu Gln Lys Pro Asn Phe Lys Ile Gly Thr Phe Met Ile Pro Gly  
 260 265 270  
 Lys Glu Lys Gly Gln Ser Leu Thr Val Gly Ala Gly Asp Leu Ala Trp  
 275 280 285  
 Ser Ile Ser Ala Thr Thr Lys His Pro Lys Glu Ala Asn Ala Phe Val  
 290 295 300  
 Glu Tyr Met Thr Arg Pro Glu Val Met Gln Lys Tyr Tyr Asp Val Asp  
 305 310 315 320  
 Gly Ser Pro Thr Ala Ile Glu Gly Val Lys Gln Ala Gly Glu Asp Ser  
 325 330 335  
 Pro Leu Ala Gly Met Thr Glu Tyr Ala Phe Thr Asp Arg His Leu Val  
 340 345 350

0076321 0330  
 T0220 12259260

Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr  
355 360 365

Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu  
370 375 380

Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp  
385 390 395

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC	60
TATTACTATT GGATTTGATA GTACTTTTGT TCCAATGGGA TTTGCTCAGA AAGATGGTTC	120
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT	180
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA	240
TCTGATTTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA	300
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC	360
AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT	420
TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA	480
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA	540
CCGTGTCTAT GCAAACCTATT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCTT	600
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTTGGAGCC CGTAAGGAAG ATACAAACTT	660
GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT	720
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG	775

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly	Lys	Asn	Ser	Ser	Glu	Thr	Ser	Gly	Asp	Asn	Trp	Ser	Lys	Tyr	Gln
1				5				10						15	

Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met



131

20

25

30

Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu  
 35 40 45  
 Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro  
 50 55 60  
 Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp  
 65 70 75 80  
 Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val  
 85 90 95  
 Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys  
 100 105 110  
 Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu  
 115 120 125  
 Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro  
 130 135 140  
 Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln  
 145 150 155 160  
 Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly  
 165 170 175  
 Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly  
 180 185 190  
 Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala  
 195 200 205  
 Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile  
 210 215 220  
 Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile  
 225 230 235 240  
 Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu  
 245 250 255  
 Gly Gln

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAAATA AAAGTTGTTG CTACAAACTC

60

AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT

120

TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180  
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGT 240  
 TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300  
 CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360  
 TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420  
 CAAAGACCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480  
 AGACAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540  
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600  
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT 660  
 TGAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720  
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780  
 CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840  
 TGACAAGATT GCTGAAGGAT TGGCAAAA 868

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val  
 1 5 10 15  
 Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp  
 20 25 30  
 Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu  
 35 40 45  
 Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu  
 50 55 60  
 Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe  
 65 70 75 80  
 Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe  
 85 90 95  
 Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu  
 100 105 110  
 Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile  
 115 120 125

Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn  
 130 135 140  
 Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu  
 145 150 155 160  
 Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala  
 165 170 175  
 Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser  
 180 185 190  
 Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu  
 195 200 205  
 Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg  
 210 215 220  
 Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg  
 225 230 235 240  
 Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln  
 245 250 255  
 Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr  
 260 265 270  
 Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala  
 275 280 285

Lys

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCGCT	60
TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC	120
AAATGAAAAG TTAATTTTGC AACGTTTGGG GAAGGAAACT GCGGTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG	300
TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTC ACGATATGGC	480
TTGGATTAAC AAAGATTGGC TTAAGAACT TGGTCTTGAA ATGCCAAAAA CTA CTGATGA	540

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA 600  
 TGAAATTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC 660  
 TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA 720  
 CTTACACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA 780  
 AAAAGGCCTG ATTGATAAAG AAGCTTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG 840  
 TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA 900  
 CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG 960  
 TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT 1020  
 AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA 1080  
 CTGGGGAAC TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA 1140  
 TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA 1200  
 AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA 1260  
 TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320  
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA 1380  
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440  
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT 1500  
 CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 515 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val  
 1 5 10 15  
 Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser  
 20 25 30  
 Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg  
 35 40 45  
 Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser  
 50 55 60  
 Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro  
 65 70 75 80  
 Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

135

85

90

95

Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val	Glu	Asp	Leu	Ile	Asp	Lys	Tyr
			100					105					110		
Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp	Glu	Lys	Pro	Glu	Tyr	Lys	Ala
		115					120					125			
Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile	Tyr	Ser	Phe	Pro	Trp	Ile	Glu
	130					135					140				
Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile	His	Ser	Val	Asn	Asp	Met	Ala
145					150					155					160
Trp	Ile	Asn	Lys	Asp	Trp	Leu	Lys	Lys	Leu	Gly	Leu	Glu	Met	Pro	Lys
				165					170					175	
Thr	Thr	Asp	Asp	Leu	Ile	Lys	Val	Leu	Glu	Ala	Phe	Lys	Asn	Gly	Asp
			180					185					190		
Pro	Asn	Gly	Asn	Gly	Glu	Ala	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ile	Ser
		195					200					205			
Gly	Asn	Gly	Asn	Glu	Asp	Phe	Lys	Phe	Leu	Phe	Ala	Ala	Phe	Gly	Ile
	210					215					220				
Gly	Asp	Asn	Asp	Asp	His	Leu	Val	Val	Gly	Asn	Asp	Gly	Lys	Val	Asp
225					230					235					240
Phe	Thr	Ala	Asp	Asn	Asp	Asn	Tyr	Lys	Glu	Gly	Val	Lys	Phe	Ile	Arg
				245					250					255	
Gln	Leu	Gln	Glu	Lys	Gly	Leu	Ile	Asp	Lys	Glu	Ala	Phe	Glu	His	Asp
			260					265					270		
Trp	Asn	Ser	Tyr	Ile	Ala	Lys	Gly	His	Asp	Gln	Lys	Phe	Gly	Val	Tyr
		275					280					285			
Phe	Thr	Trp	Asp	Lys	Asn	Asn	Val	Thr	Gly	Ser	Asn	Glu	Ser	Tyr	Asp
	290					295					300				
Val	Leu	Pro	Val	Leu	Ala	Gly	Pro	Ser	Gly	Gln	Lys	His	Val	Ala	Arg
305					310					315					320
Thr	Asn	Gly	Met	Gly	Phe	Ala	Arg	Asp	Lys	Met	Val	Ile	Thr	Ser	Val
				325					330					335	
Asn	Lys	Asn	Leu	Glu	Leu	Thr	Ala	Lys	Trp	Ile	Asp	Ala	Gln	Tyr	Ala
			340					345					350		
Pro	Leu	Gln	Ser	Val	Gln	Asn	Asn	Trp	Gly	Thr	Tyr	Gly	Asp	Asp	Lys
		355					360					365			
Gln	Gln	Asn	Ile	Phe	Glu	Leu	Asp	Gln	Ala	Ser	Asn	Ser	Leu	Lys	His
	370					375					380				
Leu	Pro	Leu	Asn	Gly	Thr	Ala	Pro	Ala	Glu	Leu	Arg	Gln	Lys	Thr	Glu
385					390					395					400
Val	Gly	Gly	Pro	Leu	Ala	Ile	Leu	Asp	Ser	Tyr	Tyr	Gly	Lys	Val	Thr
				405					410					415	
Thr	Met	Pro	Asp	Asp	Ala	Lys	Trp	Arg	Leu	Asp	Leu	Ile	Lys	Glu	Tyr

	420		425		430
Tyr Val Pro Tyr Met Ser Asn	Val Asn Asn Tyr Pro Arg Val Phe Met				
435	440	445			
Thr Gln Glu Asp Leu Asp Lys	Ile Ala His Ile Glu Ala Asp Met Asn				
450	455	460			
Asp Tyr Ile Tyr Arg Lys Arg	Ala Glu Trp Ile Val Asn Gly Asn Ile				
465	470	475	480		
Asp Thr Glu Trp Asp Asp Tyr	Lys Lys Glu Leu Glu Lys Tyr Gly Leu				
485	490	495			
Ser Asp Tyr Leu Ala Ile Lys	Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala				
500	505	510			
Asn Lys Asn					
515					

## (2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 895 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAGT TCACTGGACG AGGTCAAACCT TTCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTGCGGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCCTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA	895

## (2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser	Thr	Asn	Ser	Ser	Thr	Ser	Gln	Thr	Glu	Thr	Ser	Ser	Ser	Ala	Pro	1	5	10	15
Thr	Glu	Val	Thr	Ile	Lys	Ser	Ser	Leu	Asp	Glu	Val	Lys	Leu	Ser	Lys	20	25	30	
Val	Pro	Glu	Lys	Ile	Val	Thr	Phe	Asp	Leu	Gly	Ala	Ala	Asp	Thr	Ile	35	40	45	
Arg	Ala	Leu	Gly	Phe	Glu	Lys	Asn	Ile	Val	Gly	Met	Pro	Thr	Lys	Thr	50	55	60	
Val	Pro	Thr	Tyr	Leu	Lys	Asp	Leu	Val	Gly	Thr	Val	Lys	Asn	Val	Gly	65	70	75	80
Ser	Met	Lys	Glu	Pro	Asp	Leu	Glu	Ala	Ile	Ala	Ala	Leu	Glu	Pro	Asp	85	90	95	
Leu	Ile	Ile	Ala	Ser	Pro	Arg	Thr	Gln	Lys	Phe	Val	Asp	Lys	Phe	Lys	100	105	110	
Glu	Ile	Ala	Pro	Thr	Val	Leu	Phe	Gln	Ala	Ser	Lys	Asp	Asp	Tyr	Trp	115	120	125	
Thr	Ser	Thr	Lys	Ala	Asn	Ile	Glu	Ser	Leu	Ala	Ser	Ala	Phe	Gly	Glu	130	135	140	
Thr	Gly	Thr	Gln	Lys	Ala	Lys	Glu	Glu	Leu	Thr	Lys	Leu	Asp	Lys	Ser	145	150	155	160
Ile	Gln	Glu	Val	Ala	Thr	Lys	Asn	Glu	Ser	Ser	Asp	Lys	Lys	Ala	Leu	165	170	175	
Ala	Ile	Leu	Leu	Asn	Glu	Gly	Lys	Met	Ala	Ala	Phe	Gly	Ala	Lys	Ser	180	185	190	
Arg	Phe	Ser	Phe	Leu	Tyr	Gln	Thr	Leu	Lys	Phe	Lys	Pro	Thr	Asp	Thr	195	200	205	
Lys	Phe	Glu	Asp	Ser	Arg	His	Gly	Gln	Glu	Val	Ser	Phe	Glu	Ser	Val	210	215	220	
Lys	Glu	Ile	Asn	Pro	Asp	Ile	Leu	Phe	Val	Ile	Asn	Arg	Thr	Leu	Ala	225	230	235	240
Ile	Gly	Gly	Asp	Asn	Ser	Ser	Asn	Asp	Gly	Val	Leu	Glu	Asn	Ala	Leu	245	250	255	
Ile	Ala	Glu	Thr	Pro	Ala	Ala	Lys	Asn	Gly	Lys	Ile	Ile	Gln	Leu	Thr	260	265	270	

Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu  
 275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys  
 290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GGCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CCAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300
ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA	360
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC	420
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG	480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA	540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT	600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA	660
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA	720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC	780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG	840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA	900
CCTTGTAAC GGGTTTGCAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA	960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC	1020
AGGTGCTTTC CCAGTCCGTA CTTCAATTTGG AAAACTTTAT GAAGACAAAC GCATGGAAAC	1080
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTTGCTGA	1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC	1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA	1260
A	1261

(2) INFORMATION FOR SEQ ID NO: 26:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly 1	Asn	Ser	Gly 5	Gly	Ser	Lys	Asp	Ala 10	Lys	Ser	Gly	Gly	Asp 15	Gly	
Ala	Lys	Thr	Glu 20	Ile	Thr	Trp	Trp	Ala 25	Phe	Pro	Val	Phe	Thr 30	Gln	Glu
Lys	Thr	Gly 35	Asp	Gly	Val	Gly	Thr 40	Tyr	Glu	Lys	Ser	Ile 45	Ile	Glu	Ala
Phe 50	Glu	Lys	Ala	Asn	Pro	Asp 55	Ile	Lys	Val	Lys	Leu 60	Glu	Thr	Ile	Asp
Phe 65	Lys	Ser	Gly	Pro	Glu 70	Lys	Ile	Thr	Thr 75	Ala	Ile	Glu	Ala	Gly 80	Thr
Ala	Pro	Asp	Val 85	Leu	Phe	Asp	Ala	Pro	Gly 90	Arg	Ile	Ile	Gln 95	Tyr	Gly
Lys	Asn	Gly 100	Lys	Leu	Ala	Glu	Leu	Asn 105	Asp	Leu	Phe	Thr	Asp 110	Glu	Phe
Val	Lys	Asp 115	Val	Asn	Asn	Glu	Asn 120	Ile	Val	Gln	Ala	Ser 125	Lys	Ala	Gly
Asp 130	Lys	Ala	Tyr	Met	Tyr	Pro 135	Ile	Ser	Ser	Ala	Pro 140	Phe	Tyr	Met	Ala
Met 145	Asn	Lys	Lys	Met	Leu 150	Glu	Asp	Ala	Gly	Val 155	Ala	Asn	Leu	Val	Lys 160
Glu	Gly	Trp	Thr 165	Thr	Asp	Asp	Phe	Glu	Lys 170	Val	Leu	Lys	Ala	Leu 175	Lys
Asp	Lys	Gly 180	Tyr	Thr	Pro	Gly	Ser 185	Leu	Phe	Ser	Ser	Gly 190	Gln	Gly	Gly
Asp	Gln	Gly 195	Thr	Arg	Ala	Phe	Ile 200	Ser	Asn	Leu	Tyr	Ser 205	Gly	Ser	Val
Thr 210	Asp	Glu	Lys	Val	Ser	Lys 215	Tyr	Thr	Thr	Asp	Asp 220	Pro	Lys	Phe	Val
Lys 225	Gly	Leu	Glu	Lys	Ala 230	Thr	Ser	Trp	Ile	Lys 235	Asp	Asn	Leu	Ile	Asn 240
Asn	Gly	Ser	Gln	Phe 245	Asp	Gly	Gly	Ala	Asp 250	Ile	Gln	Asn	Phe 255	Ala	Asn
Gly	Gln	Thr 260	Ser	Tyr	Thr	Ile	Leu	Trp 265	Ala	Pro	Ala	Gln	Asn 270	Gly	Ile

Gln Ala Lys Leu Leu Glu Ala Ser Lys Val Glu Val Val Glu Val Pro  
275 280 285

Phe Pro Ser Asp Glu Gly Lys Pro Ala Leu Glu Tyr Leu Val Asn Gly  
290 295 300

Phe Ala Val Phe Asn Asn Lys Asp Asp Lys Lys Val Ala Ala Ser Lys  
305 310 315 320

Lys Phe Ile Gln Phe Ile Ala Asp Asp Lys Glu Trp Gly Pro Lys Asp  
325 330 335

Val Val Arg Thr Gly Ala Phe Pro Val Arg Thr Ser Phe Gly Lys Leu  
340 345 350

Tyr Glu Asp Lys Arg Met Glu Thr Ile Ser Gly Trp Thr Gln Tyr Tyr  
355 360 365

Ser Pro Tyr Tyr Asn Thr Ile Asp Gly Phe Ala Glu Met Arg Thr Leu  
370 375 380

Trp Phe Pro Met Leu Gln Ser Val Ser Asn Gly Asp Glu Lys Pro Ala  
385 390 395 400

Asp Ala Leu Lys Ala Phe Thr Glu Lys Ala Asn Glu Thr Ile Lys Lys  
405 410 415

Ala Met Lys Gln  
420

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAA ATGAAGATGG AGAACTAAG ACAGAACAGA CAGCCAAAGC	60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCAG AAGAAAGCAG AAGTGGTCAA	120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA	180
CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT	240
CAAACTCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT	300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC	360
AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT	420
TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT	480
GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC	540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC	600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GGCGGAGACT ACGTCGAT	658

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
1      5      10      15
Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
20      25      30
Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
35      40      45
Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
50      55      60
Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
65      70      75      80
Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His
85      90      95
Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp
100     105     110
Tyr Val Asn Gln Asp Gly Lys Ala Ala Ala Asp Arg Tyr Ser Ala Arg
115     120     125
Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly
130     135     140
Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu
145     150     155     160
Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys
165     170     175
Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val
180     185     190
Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu
195     200     205
Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp
210     215

```

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGAAAA 60  
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGGTTGTGG 120  
GAAATCAACA CTCATTAAAA CCTTGTCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180  
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240  
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300  
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGAAAA GATGACCTTG AAATAATAAA 360  
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420  
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480  
ACTTTTAGAT GAGCCAACTA CTTACTTGGA TATCTCATAT CAAATAGAAC TATTAGACCT 540  
CTTGACTGAT CTAAACCAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA 600  
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660  
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720  
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA 780  
TGTTAACTCT 790

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile  
1 5 10 15  
Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val  
20 25 30  
Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu  
35 40 45  
Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys  
50 55 60  
Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile  
65 70 75 80  
Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu  
85 90 95

— Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly  
                             100                            105                            110  
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val  
                             115                            120                            125  
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg  
                             130                            135                            140  
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu  
                             145                            150                            155                            160  
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu  
                             165                            170                            175  
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile  
                             180                            185                            190  
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr  
                             195                            200                            205  
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu  
                             210                            215                            220  
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala  
                             225                            230                            235                            240  
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile  
                             245                            250                            255  
 Gly Lys His His Val Ser  
                             260

## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG	60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC	120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA	180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG	240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT	300
GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC	360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT	420
GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC	480
AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT	540

TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600  
 ACTTTTCAAA GAACAAGCTG ATGAAAAC TC AAAACAATGG TACAACATCA TTGTTGCAAA 660  
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720  
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG 780  
 G 781

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr  
 1 5 10 15  
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu  
 20 25 30  
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp  
 35 40 45  
 Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn  
 50 55 60  
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly  
 65 70 75 80  
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu  
 85 90 95  
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp  
 100 105 110  
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu  
 115 120 125  
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp  
 130 135 140  
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro  
 145 150 155 160  
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser  
 165 170 175  
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu  
 180 185 190  
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu  
 195 200 205

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Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu  
 210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His  
 225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp  
 245 250 255

Gln Pro Val Trp  
 260

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA 60

TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC 120

CATCCAAAAA GTTTTTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA 180

TACTATTGCC GAAGAAAAAA AACAATATGG CGAAACTAC CAACGTGTCT TGTCACAAGC 240

AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC 300

AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA 360

GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA 420

AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC 480

AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA 540

AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTGCTTTT AGATGTGGGA TGGTGTCTTCT 600

GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG 640

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val  
 1 5 10 15

Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala

146

20

25

30

Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln  
 35 40 45  
 Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu  
 50 55 60  
 Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala  
 65 70 75 80  
 Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu  
 85 90 95  
 Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu  
 100 105 110  
 Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln  
 115 120 125  
 Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys  
 130 135 140  
 Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser  
 145 150 155 160  
 Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser  
 165 170 175  
 Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala  
 180 185 190  
 Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly  
 195 200 205  
 Thr Pro Ser Leu Gln  
 210

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC 60  
 TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTTCAGTG 120  
 TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA 180  
 ACCACTGAAA GATTTTtagag CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG 240  
 TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA 300  
 ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG 360  
 CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG 420



ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480  
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540  
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600  
 CCGTGTAAT GGTAAATGGTG AATGGGTAAA C 631

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr  
 1 5 10 15  
 Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly  
 20 25 30  
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu  
 35 40 45  
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp  
 50 55 60  
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly  
 65 70 75 80  
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys  
 85 90 95  
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr  
 100 105 110  
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly  
 115 120 125  
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe  
 130 135 140  
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr  
 145 150 155 160  
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys  
 165 170 175  
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val  
 180 185 190  
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp  
 195 200 205  
 Val Asn  
 210

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## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC 60  
 AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC 120  
 AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT 180  
 AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA 240  
 AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT 300  
 TGAAGAAGCT AAGAAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC 360  
 CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TAAAAAAGC 420  
 GGAGCTTGAA CTAGTAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA 480  
 AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC 540  
 AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA 600  
 AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC 660  
 AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA 720  
 AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA 780  
 ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA 840  
 AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA 900  
 CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA 960  
 CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA 1020  
 CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA 1080  
 CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA 1140  
 CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA 1200  
 TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA 1260  
 AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT 1320  
 AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC 1360

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp	Glu	Gln	Lys	Ile	Lys	Gln	Ala	Glu	Ala	Glu	Val	Glu	Ser	Lys	Gln	1	5	10	15
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Lys	Ile	Lys	Thr	Asp	Arg	Glu	Glu	Ala	20	25	30	
Glu	Glu	Glu	Ala	Lys	Arg	Arg	Ala	Asp	Ala	Lys	Glu	Gln	Gly	Lys	Pro	35	40	45	
Lys	Gly	Arg	Ala	Lys	Arg	Gly	Val	Pro	Gly	Glu	Leu	Ala	Thr	Pro	Asp	50	55	60	
Lys	Lys	Glu	Asn	Asp	Ala	Lys	Ser	Ser	Asp	Ser	Ser	Val	Gly	Glu	Glu	65	70	75	80
Thr	Leu	Pro	Ser	Pro	Ser	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	85	90	95	
Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Glu	Asp	Gln	Lys	Glu	100	105	110	
Glu	Asp	Arg	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	115	120	125	
Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu	Leu	Glu	Leu	130	135	140	
Val	Lys	Glu	Glu	Ala	Lys	Glu	Pro	Arg	Asn	Glu	Glu	Lys	Val	Lys	Gln	145	150	155	160
Ala	Lys	Ala	Glu	Val	Glu	Ser	Lys	Lys	Ala	Glu	Ala	Thr	Arg	Leu	Glu	165	170	175	
Lys	Ile	Lys	Thr	Asp	Arg	Lys	Lys	Ala	Glu	Glu	Glu	Ala	Lys	Arg	Lys	180	185	190	
Ala	Ala	Glu	Glu	Asp	Lys	Val	Lys	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Gln	195	200	205	
Pro	Ala	Pro	Ala	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Lys	Pro	210	215	220	
Glu	Asn	Pro	Ala	Glu	Gln	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Asp	Gln	Gln	225	230	235	240
Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	Leu	245	250	255	
Thr	Gln	Gln	Gln	Pro	Pro	Lys	Thr	Glu	Lys	Pro	Ala	Gln	Pro	Ser	Thr	260	265	270	
Pro	Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	275	280	285	

150

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp  
290 295 300

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn  
305 310 315 320

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly  
325 330 335

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser  
340 345 350

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn  
355 360 365

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp  
370 375 380

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp  
385 390 395 400

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser  
405 410 415

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly  
420 425 430

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn  
435 440 445

Gly Glu Trp Val Asn  
450

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 amino acids

- (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys Gly Glu Glu Glu Thr Lys Lys Thr Gln Ala Ala Gln Gln Pro Lys  
 1                      5                      10                      15  
 Gln Gln Thr Thr Val Gln Gln Ile Ala Val Gly Lys Asp Ala Pro Asp  
                     20                      25                      30  
 Phe Thr Leu Gln Ser Met Asp Gly Lys Glu Val Lys Leu Ser Asp Phe  
                     35                      40                      45  
 Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys Gly Pro  
                     50                      55                      60  
 Cys Lys Lys Ser Met Pro Glu Leu Met Glu Leu Ala Ala Lys Pro Asp  
                     65                      70                      75                      80  
 Arg Asp Phe Glu Ile Leu Thr Val Ile Ala Pro Gly Ile Gln Gly Glu  
                     85                      90                      95  
 Lys Thr Val Glu Gln Phe Pro Gln Trp Phe Gln Glu Gln Gly Tyr Lys  
                     100                      105                      110  
 Asp Ile Pro Val Leu Tyr Asp Thr Lys Ala Thr Thr Ser Lys Leu Ile  
                     115                      120                      125  
 Lys Phe Glu Ala Phe Leu Gln Asn Ile  
                     130                      135

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1462 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTT 60  
 TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA 120  
 TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAA GCTAAAGCCA TTGATGAAGC 180  
 tGGAATTGAT GCTGACAATG TCCTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC 240  
 TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT 300  
 TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA 360  
 CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA 420  
 CGCTTGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTCTGCCG CAGCTGTAGC 480

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CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540  
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAQ GTTTCGGTCT 600  
 CATTCGCTTT GGTAGTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660  
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720  
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780  
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840  
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900  
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960  
 CTTCGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020  
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080  
 TTTCAGTCTT TCATCAGGTT ACTATGATGC CTAATAAAA AAGGCTGGTC AAGTCCGTAC 1140  
 CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200  
 TGCTCCAAGT GTTGCCTATG ACTTGGATTC TCTCAACCAT GACCCAGTTG CCATGTACTT 1260  
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCTCTG 1320  
 TGGATTCTCT CAAGGTCTAC CTGTCGGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380  
 AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440  
 CGTGATTTTT GGAGGTGACA AC 1462

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Phe Asn Asn Lys Thr Ile Glu Glu Leu His Asn Leu Leu Val Ser  
 1 5 10 15

Lys Glu Ile Ser Ala Thr Glu Leu Thr Gln Ala Thr Leu Glu Asn Ile  
 20 25 30

Lys Ser Arg Glu Glu Ala Leu Asn Ser Phe Val Thr Ile Ala Glu Glu  
 35 40 45

Gln Ala Leu Val Gln Ala Lys Ala Ile Asp Glu Ala Gly Ile Asp Ala  
 50 55 60

Asp Asn Val Leu Ser Gly Ile Pro Leu Ala Val Lys Asp Asn Ile Ser  
 65 70 75 80

Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr  
 85 90 95  
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly  
 100 105 110  
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly  
 115 120 125  
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His  
 130 135 140  
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala  
 145 150 155 160  
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile  
 165 170 175  
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr  
 180 185 190  
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp  
 195 200 205  
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Asn Ala Leu Leu Leu  
 210 215 220  
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val  
 225 230 235 240  
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met  
 245 250 255  
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu  
 260 265 270  
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly  
 275 280 285  
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala  
 290 295 300  
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg  
 305 310 315 320  
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu  
 325 330 335  
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val  
 340 345 350  
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr  
 355 360 365  
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln  
 370 375 380  
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr  
 385 390 395 400  
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val  
 405 410 415

0076527 1 012204  
 102210 1255260

Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly  
                   420                                  425                                  430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val  
                   435                                  440                                  445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln  
                   450                                  455                                  460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro  
                   465                                  470                                  475                                  480

Val Ile Phe Gly Gly Asp Asn  
                                   485

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAAC TAC AAGTCGGCGA CAAGGCGCTT GATTTTTCTC TTACTACAAC	60
AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT	120
TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC	180
TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG	240
TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC	300
TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT	360
TGTCCTCGAT ACTGACAATA CGATTGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA	420
GCCAAACTTC GAA	433

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser	
1                                  5                                  10                                  15	
Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly	
20                                  25                                  30	
Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys	



35

40

45

Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn  
 50 55 60

Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg  
 65 70 75 80

Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr  
 85 90 95

Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp  
 100 105 110

His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile  
 115 120 125

Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu  
 130 135 140

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA 60

ACAAGACGTT CCCAATTTTG GTTACAAnGA TCCAAGACC GGTACTTATT CTGGTATCGA 120

AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT 180

TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC 240

CTTTACCATC ACGGACGAAC GCAAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA 300

CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAATCAAA AAGATTGAGG ACCTAAACGG 360

CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA 420

AAAGAAAGGT CTGAAGTTTA AATTCGTGCGA ACTTGTTCC TACCCAGAAT TGATTACTTC 480

CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC 540

TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC 600

CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA 660

GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC 720

AGAT 724

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val  
 1                      5                      10                      15  
 Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys  
                     20                      25                      30  
 Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala  
                     35                      40                      45  
 Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr  
                     50                      55                      60  
 Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr  
                     65                      70                      75                      80  
 Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro  
                     85                      90                      95  
 Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile  
                     100                      105                      110  
 Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly  
                     115                      120                      125  
 Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu  
                     130                      135                      140  
 Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser  
                     145                      150                      155                      160  
 Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu  
                     165                      170                      175  
 Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys  
                     180                      185                      190  
 Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn  
                     195                      200                      205  
 Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu  
                     210                      215                      220  
 Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala  
                     225                      230                      235                      240  
 Asp

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTG TtgACTTTTCA CTATCTCTCA 60  
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120  
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAT TTGGTGAAGA 180  
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240  
 AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAAC'TTCAA TGGAAAAAGG 300  
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360  
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCGAAGA 420  
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480  
 AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCATC GACGGTGTG AATTTGACGG 540  
 TGGAAAAGGT GAAAACTTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600  
 AGACCAATTG GTAGGTCCT CAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCCCAGA 660  
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720  
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAAGACA TTGATGAAGA 780  
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840  
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900  
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960  
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020  
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080  
 CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140  
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCAACAAG TTCAAAACTT 1200  
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260  
 AAGCACAGCA ACAGTAAAA 1279

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

1	5	10	15
Thr Ile Ser Gln Asp Gln Ile Lys Pro Glu Leu Asp Arg Val Phe Lys	20	25	30
Ser Val Lys Lys Ser Leu Asn Val Pro Gly Phe Arg Lys Gly His Leu	35	40	45
Pro Arg Pro Ile Phe Asp Gln Lys Phe Gly Glu Glu Ala Leu Tyr Gln	50	55	60
Asp Ala Met Asn Ala Leu Leu Pro Asn Ala Tyr Glu Ala Ala Val Lys	65	70	75
Glu Ala Gly Leu Glu Val Val Ala Gln Pro Lys Ile Asp Val Thr Ser	85	90	95
Met Glu Lys Gly Gln Asp Trp Val Ile Thr Ala Glu Val Val Thr Lys	100	105	110
Pro Glu Val Lys Leu Gly Asp Tyr Lys Asn Leu Glu Val Ser Val Asp	115	120	125
Val Glu Lys Glu Val Thr Asp Ala Asp Val Glu Glu Arg Ile Glu Arg	130	135	140
Glu Arg Asn Asn Leu Ala Glu Leu Val Ile Lys Glu Ala Ala Ala Glu	145	150	155
Asn Gly Asp Thr Val Val Ile Asp Phe Val Gly Ser Ile Asp Gly Val	165	170	175
Glu Phe Asp Gly Gly Lys Gly Glu Asn Phe Ser Leu Gly Leu Gly Ser	180	185	190
Gly Gln Phe Ile Pro Gly Phe Glu Asp Gln Leu Val Gly His Ser Ala	195	200	205
Gly Glu Thr Val Asp Val Ile Val Thr Phe Pro Glu Asp Tyr Gln Ala	210	215	220
Glu Asp Leu Ala Gly Lys Glu Ala Lys Phe Val Thr Thr Ile His Glu	225	230	235
Val Lys Ala Lys Glu Val Pro Ala Leu Asp Asp Glu Leu Ala Lys Asp	245	250	255
Ile Asp Glu Glu Val Glu Thr Leu Ala Asp Leu Lys Glu Lys Tyr Ser	260	265	270
Lys Glu Leu Ala Ala Ala Lys Glu Glu Ala Tyr Lys Asp Ala Val Glu	275	280	285
Gly Ala Ala Ile Asp Thr Ala Val Glu Asn Ala Glu Ile Val Glu Leu	290	295	300
Pro Glu Glu Met Ile His Glu Glu Val His Arg Ser Val Asn Glu Phe	305	310	315
Leu Gly Asn Leu Gln Arg Gln Gly Ile Asn Pro Asp Met Tyr Phe Gln	325	330	335
Ile Thr Gly Thr Thr Gln Glu Asp Leu His Asn Gln Tyr Gln Ala Glu			

350.

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys  
420 425

(A) LENGTH: 490 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TGGTCAAAAG	GAAAGTCAGA	CAGGAAAGGG	GATGAAAATT	GTGACCAGTT	TTTATCCTAT	60
CTACGCTATG	GTTAAGGAAG	TATCTGGTGA	CTTGAATGAT	GTTCGGATGA	TTCAGTCAAG	120
TAGTGGTATT	CACTCCTTTG	AACCTTCGGC	AAATGATATC	GCAGCCATCT	ATGATGCAGA	180
TGTCTTTGTT	TACCATTCTC	ATACACTCGA	ATCTTGGGCA	GGAAGTCTGG	ATCCAAATCT	240
AAAAAAATCC	AAAGTGAAGG	TCTTAGAGGC	TTCTGAGGGA	ATGACCTTGG	AACGTGTCCC	300
TGGACTAGAG	GATGTGGAAG	CAGGGGATGG	AGTTGATGAA	AAAACGCTCT	ATGACCCTCA	360
CACATGGCTA	GATCCTGAAA	AAGCTGGAGA	AGAAGCCCAA	ATTATCGCTG	ATAAACTTTC	420
AGAGGTGGAT	AGTGAGCATA	AAGAGACTTA	TCAAAAAAAT	GCGCAACCTT	TATCAAAAAA	480
GCTCAGGAAT						490

(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser  
 1 5 10 15

160

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn  
 20 25 30  
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro  
 35 40 45  
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr  
 50 55 60  
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu  
 65 70 75 80  
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu  
 85 90 95  
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp  
 100 105 110  
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala  
 115 120 125  
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser  
 130 135 140  
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys  
 145 150 155 160  
 Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT	60
GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG	120
TTTTGGTGCC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG	180
TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT	240
TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT	300
TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC	360
AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA	420
CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA	480
TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC	540
AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGCAGGAT ATTTATGATT TCCCCCGTGC	600
CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA	660

TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720  
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780  
 TCCTGTAAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840  
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900  
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960  
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser  
 1 5 10 15  
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala  
 20 25 30  
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val  
 35 40 45  
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala  
 50 55 60  
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val  
 65 70 75 80  
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala  
 85 90 95  
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn  
 100 105 110  
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu  
 115 120 125  
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val  
 130 135 140  
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp  
 145 150 155 160  
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu  
 165 170 175  
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln  
 180 185 190  
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn		
210	215	220
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser		
225	230	235 240
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala		
	245	250 255
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala		
	260	265 270
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val		
	275	280 285
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met		
	290	295 300
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly		
305	310	315 320
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu		
	325	330 335

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACCTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTTCTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACCTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTAACCTAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCTC CAACTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780



TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840  
 TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAAACTAAAG TTCTTGACGT 900  
 TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACTACTGC 960  
 ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC 1000

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala  
 1 5 10 15  
 Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn  
 20 25 30  
 Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr  
 35 40 45  
 Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe  
 50 55 60  
 Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu  
 65 70 75 80  
 Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr  
 85 90 95  
 Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly  
 100 105 110  
 Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr  
 115 120 125  
 Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val  
 130 135 140  
 Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys  
 145 150 155 160  
 Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile  
 165 170 175  
 His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly  
 180 185 190  
 Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn  
 195 200 205  
 Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn  
 210 215 220

Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser  
 225 230 235 240  
 Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu  
 245 250 255  
 Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr  
 260 265 270  
 Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser  
 275 280 285  
 — Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln  
 290 295 300  
 Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala  
 305 310 315 320  
 Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys  
 325 330

## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA	60
TATAGATGGA AAACAAGCGA CGCAAAAAC GGAGAATTTG ACTCCTGATG AGGTTAGCAA	120
GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC	180
TTCACATGGC GACCACTATC ATTATTACAA TGGTAAGGTT CCTTATGACG CTATCATCAG	240
TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA	300
GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC	360
TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAC AAGAGCATAG	420
TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCCTTG CACGTTTCGCA	480
AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC	540
TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCTA AGAATGAGTT	600
ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCTATCT GGTGAGGAA ATCTGTCAAA	660
TTCAAGAACC TATCGCCGAC AAAATAGCGA TAACACTTCA AGAACAAACT GGGTACCTTC	720
TGTAAGCAAT CCAGGAATA CAAATACTAA CACAAGCAAC AACAGCAACA CTAACAGTCA	780
AGCAAGTCAA AGTAATGACA TTGATAGTCT CTTGAAACAG CTCTACAAAC TGCCTTTGAG	840
TCAACGACAT GTAGAATCTG ATGGCCTTGT CTTTGATCCA GCACAAATCA CAAGTCGAAC	900
AGCTAGAGGT GTTGCACTGC CACACGGAGA TCATTACCAC TTCATCCCTT ACTCTCAAT	960

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020  
 GGTACCAGAT TCAAGGCCAG AACAACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080  
 CCCGCAACCT GCACCAAATC TTAAATAGA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT 1140  
 ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200  
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAAGAGAG 1260  
 TGTTCACAC ACTTTAACTG CTAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320  
 TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNA AATAAGGGTCG 1380  
 TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440  
 TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG 1500  
 ACTTGGCAAA CCAAATTCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560  
 AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTTGAT GAACATGATA TAATCAGTGA 1620  
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680  
 CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740  
 TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAGTGA GATAGTGCAG CAGCTATTTA 1800  
 CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860  
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT 1920  
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGGAAGA 1980  
 TTTGTTTGCG ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040  
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100  
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160  
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220  
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAACT CTAGCTGGTT TACGAAATAA 2280  
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340  
 GTTGTTAAAA GGAAGTAATC CTTATCTGT AAGTAAGGAA AAAATAAAC 2389

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

1		5						10				15				
Arg	Val	Ser	Tyr	Ile	Asp	Gly	Lys	Gln	Ala	Thr	Gln	Lys	Thr	Glu	Asn	
		20						25					30			
Leu	Thr	Pro	Asp	Glu	Val	Ser	Lys	Arg	Glu	Gly	Ile	Asn	Ala	Glu	Gln	
		35					40					45				
Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His	Gly	Asp	
	50					55					60					
His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr	Asp	Ala	Ile	Ile	Ser	
65					70					75					80	
Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Lys	Leu	Lys	Asp	Glu	Asp	
				85					90					95		
Ile	Val	Asn	Glu	Val	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asp	Gly	Lys	
			100					105						110		
Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Val	Arg	Thr	
		115					120					125				
Lys	Glu	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His	Ser	Gln	His	Arg	Glu	
	130					135						140				
Gly	Gly	Thr	Pro	Arg	Asn	Asp	Gly	Ala	Val	Ala	Leu	Ala	Arg	Ser	Gln	
145					150					155					160	
Gly	Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile	
				165					170					175		
Ile	Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	
			180					185						190		
His	Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	
		195					200					205				
Glu	Ala	Phe	Leu	Ser	Gly	Arg	Gly	Asn	Leu	Ser	Asn	Ser	Arg	Thr	Tyr	
	210					215					220					
Arg	Arg	Gln	Asn	Ser	Asp	Asn	Thr	Ser	Arg	Thr	Asn	Trp	Val	Pro	Ser	
225					230					235					240	
Val	Ser	Asn	Pro	Gly	Thr	Thr	Asn	Thr	Asn	Thr	Ser	Asn	Asn	Ser	Asn	
				245					250					255		
Thr	Asn	Ser	Gln	Ala	Ser	Gln	Ser	Asn	Asp	Ile	Asp	Ser	Leu	Leu	Lys	
			260					265					270			
Gln	Leu	Tyr	Lys	Leu	Pro	Leu	Ser	Gln	Arg	His	Val	Glu	Ser	Asp	Gly	
		275					280					285				
Leu	Val	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala	Arg	Gly	Val	
	290					295					300					
Ala	Val	Pro	His	Gly	Asp	His	Tyr	His	Phe	Ile	Pro	Tyr	Ser	Gln	Met	
305					310					315					320	
Ser	Glu	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu	Arg	Tyr	Arg	
				325				330					335			
Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro	Ser	Pro	Gln	

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167

340

345

350

Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys  
355 360 365

Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly  
370 375 380

Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala  
385 390 395 400

Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser  
405 410 415

Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val  
420 425 430

Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr  
435 440 445

Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe  
450 455 460

Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn  
465 470 475 480

Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr  
485 490 495

His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu  
500 505 510

Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp  
515 520 525

Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala  
530 535 540

Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser  
545 550 555 560

Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys  
565 570 575

Gly Ile Leu Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr  
580 585 590

Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg  
595 600 605

Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val  
610 615 620

Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile  
625 630 635 640

Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr  
645 650 655

—Thr—Leu—Glu—Asp—Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro  
660 665 670

Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His

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FOOTNOTES

675	680	685
Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys		
690	695	700
Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro		
705	710	715
Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val		
	725	730
Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu		
	740	745
Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn		
	755	760
Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly		
	770	775
Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn		
	785	790
		795

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA	60
TAGTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TGCGTTTTGT	120
TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATTCTG CGGTATTAGC	180
TGAGAAATAC AATCGTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT	240
TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA	300
TGTTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA	360
TTTTAATGGA GACCAGTTGA CTAGTTTTCT GAAACATCAA TCTGGGGATC AGGCTAGTCA	420
ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA	480
GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC	540
TCGTTTTAAT GAACGCCAAG CTTCTTTTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA	600
CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC	660
AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT	720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTG AAGAAATTAA AGGATTCTCA	780
GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA	840

(2) INFORMATION FOR SEQ ID NO:58:

(A) LENGTH: 393 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr	Glu	Met	His	His	Asn	Leu	Gly	Ala	Glu	Lys	Arg	Ser	Ala	Val	Ala
1				5					10					15	
Thr	Thr	Ile	Asp	Ser	Phe	Lys	Glu	Arg	Ser	Gln	Lys	Val	Arg	Ala	Leu
		20					25					30			
Ser	Asp	Pro	Asn	Val	Arg	Phe	Val	Pro	Phe	Phe	Gly	Ser	Ser	Glu	Trp
	35						40				45				
Leu	Arg	Phe	Asp	Gly	Ala	His	Ser	Ala	Val	Leu	Ala	Glu	Lys	Tyr	Asn
	50					55					60				
Arg	Ser	Tyr	Arg	Pro	Tyr	Leu	Leu	Gly	Gln	Gly	Gly	Ala	Ala	Ser	Leu
65					70				75						80
Asn	Gln	Tyr	Phe	Gly	Met	Gln	Gln	Met	Leu	Pro	Gln	Leu	Glu	Asn	Lys
			85						90					95	
Gln	Val	Val	Tyr	Val	Ile	Ser	Pro	Gln	Trp	Phe	Ser	Lys	Asn	Gly	Tyr
		100						105					110		
Asp	Pro	Ala	Ala	Phe	Gln	Gln	Tyr	Phe	Asn	Gly	Asp	Gln	Leu	Thr	Ser
		115					120					125			
Phe	Leu	Lys	His	Gln	Ser	Gly	Asp	Gln	Ala	Ser	Gln	Tyr	Ala	Ala	Thr
	130					135					140				
Arg	Leu	Leu	Gln	Gln	Phe	Pro	Asn	Val	Ala	Met	Lys	Asp	Leu	Val	Gln
145					150					155					160
Lys	Leu	Ala	Ser	Lys	Glu	Glu	Leu	Ser	Thr	Ala	Asp	Asn	Glu	Met	Ile
				165					170					175	
Glu	Leu	Leu	Ala	Arg	Phe	Asn	Glu	Arg	Gln	Ala	Ser	Phe	Phe	Gly	Gln
			180					185					190		
Phe	Ser	Val	Arg	Gly	Tyr	Val	Asn	Tyr	Asp	Lys	His	Val	Ala	Lys	Tyr
		195					200					205			

Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val  
 210 215 220  
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met  
 225 230 235 240  
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu  
 245 250 255  
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn  
 260 265 270  
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro  
 275 280 285  
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly  
 290 295 300  
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln  
 305 310 315 320  
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly  
 325 330 335  
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly  
 340 345 350  
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr  
 355 360 365  
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp  
 370 375 380  
 Ala Thr Tyr Asp Gly Asp Val Lys Glu  
 385 390

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTAATATCAA	300
GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420



AAAACTTTCC GCTTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGA CTGAGAC 480  
 TTCCTTCAGT CCAGTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540  
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600  
 TGA ACTGATT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660  
 GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720  
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780  
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840  
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT 900  
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960  
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020  
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080  
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAT GAGGAATTGA CCTTTAAAT 1140  
 GGCCCGCAAG GAGGAACTTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200  
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260  
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320  
 CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCATTAC ACAGGACAAA AGACCCTCCG 1380  
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln  
 1 5 10 15

Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu  
 20 25 30

Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys  
 35 40 45

His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu  
 50 55 60

Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu  
 65 70 75 80

Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

85

90

95

Phe	Thr	Ile	Lys	Asp	Glu	Lys	Leu	Phe	Glu	Ile	Leu	Gln	Thr	Gln	Glu		
			100					105					110				
Leu	Thr	Ala	Lys	Asn	Leu	Gln	Ser	Leu	Phe	Gln	Gly	Leu	Gly	Arg	Asp		
		115					120					125					
Thr	Ala	Asn	Glu	Leu	Glu	Arg	Ile	Leu	Val	Ser	Glu	Lys	Leu	Ser	Ala		
	130					135					140						
Phe	Arg	Asn	Phe	Phe	Asn	Gln	Glu	Thr	Lys	Pro	Cys	Leu	Thr	Glu	Thr		
145					150				155						160		
Ser	Phe	Ser	Pro	Val	Pro	Phe	Ala	Asn	Gln	Val	Gly	Glu	Pro	Phe	Ala		
				165				170						175			
Asn	Leu	Ser	Asp	Leu	Leu	Asp	Thr	Tyr	Tyr	Lys	Asp	Lys	Ala	Glu	Arg		
			180					185					190				
Asp	Arg	Val	Lys	Gln	Gln	Ala	Ser	Glu	Leu	Ile	Arg	Arg	Val	Glu	Asn		
		195					200					205					
Glu	Leu	Gln	Lys	Asn	Arg	His	Lys	Leu	Lys	Lys	Gln	Glu	Lys	Glu	Leu		
210						215					220						
Leu	Ala	Thr	Asp	Asn	Ala	Glu	Glu	Phe	Arg	Gln	Lys	Gly	Glu	Leu	Leu		
225					230					235					240		
Thr	Thr	Phe	Leu	His	Gln	Val	Pro	Asn	Asp	Gln	Asp	Gln	Val	Ile	Leu		
				245					250					255			
Asp	Asn	Tyr	Tyr	Thr	Asn	Gln	Pro	Ile	Met	Ile	Ala	Leu	Asp	Lys	Ala		
			260					265					270				
Leu	Thr	Pro	Asn	Gln	Asn	Ala	Gln	Arg	Tyr	Phe	Lys	Arg	Tyr	Gln	Lys		
		275					280					285					
Leu	Lys	Glu	Ala	Val	Lys	Tyr	Leu	Thr	Asp	Leu	Ile	Glu	Glu	Thr	Lys		
290						295					300						
Ala	Thr	Ile	Leu	Tyr	Leu	Glu	Ser	Val	Glu	Thr	Val	Leu	Asn	Gln	Ala		
305					310					315					320		
Gly	Leu	Glu	Glu	Ile	Ala	Glu	Ile	Arg	Glu	Glu	Leu	Ile	Gln	Thr	Gly		
				325					330					335			
Phe	Ile	Arg	Arg	Arg	Gln	Arg	Glu	Lys	Ile	Gln	Lys	Arg	Lys	Lys	Leu		
			340					345					350				
Glu	Gln	Tyr	Leu	Ala	Ser	Asp	Gly	Lys	Thr	Ile	Ile	Tyr	Val	Gly	Arg		
		355					360					365					
Asn	Asn	Leu	Gln	Asn	Glu	Glu	Leu	Thr	Phe	Lys	Met	Ala	Arg	Lys	Glu		
		370				375					380						
Glu	Leu	Trp	Phe	His	Ala	Lys	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile		
385					390					395					400		
Ser	Gly	Asn	Leu	Asp	Pro	Ser	Asp	Ala	Val	Lys	Thr	Asp	Ala	Ala	Glu		
				405					410					415			
Leu	Ala	Ala	Tyr	Phe	Ser	Gln	Gly	Arg	Leu	Ser	Asn	Leu	Val	Gln	Val		

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173

420

425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro  
 435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp  
 450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser  
 465 470

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA 60  
 AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC 120  
 CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC 180  
 ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG 240  
 TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA 300  
 AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT 360  
 TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT 420  
 AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT 480  
 CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA 540  
 TGCC 544

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys  
 1 5 10 15

Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn  
 20 25 30

Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln

35

40

45

Ile Val Ser Ser ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg  
 50 55 60

Glu Val Val Gln ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys  
 65 70 75 80

Val Ala Gly His Thr Ala Phe Ser ile Lys Gln ile Gln Met Asn Asp  
 85 90 95

Asp Leu ile Gln Ala Leu Arg Asn Arg Thr Pro ile Glu Thr Asp Pro  
 100 105 110

Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val ile Asn Thr Lys  
 115 120 125

Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr  
 130 135 140

Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala ile  
 145 150 155 160

Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro ile Asn Pro Glu  
 165 170 175

Leu Gln Pro Tyr Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA 60

GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA 120

CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA 180

GTATGTCAGC CGTGGTGGTT TGAAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT 240

GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT 300

ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGA 360

ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCCGCT ATGCTGAAAA 420

GACTGATTTC GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG 480

TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT 540

CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC 600

TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC 660

AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTTCAGC 720  
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780  
 AGAGAGGGCG CATAGTCAAT TAAAAATGA A 811

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Lys Glu Arg Val Asp Val Leu Ala Tyr Lys Gln Gly Leu Phe Glu  
 1 5 10 15  
 Thr Arg Glu Gln Ala Lys Arg Gly Val Met Ala Gly Leu Val Val Ala  
 20 25 30  
 Val Leu Asn Gly Glu Arg Phe Asp Lys Pro Gly Glu Lys Ile Pro Asp  
 35 40 45  
 Asp Thr Glu Leu Lys Leu Lys Gly Glu Lys Leu Lys Tyr Val Ser Arg  
 50 55 60  
 Gly Gly Leu Lys Leu Glu Lys Ala Leu Gln Val Phe Asp Leu Ser Val  
 65 70 75 80  
 Asp Gly Ala Thr Thr Ile Asp Ile Gly Ala Ser Thr Gly Gly Phe Thr  
 85 90 95  
 Asp Val Met Leu Gln Asn Ser Ala Lys Leu Val Phe Ala Val Asp Val  
 100 105 110  
 Gly Thr Asn Gln Leu Ala Trp Lys Leu Arg Gln Asp Pro Arg Val Val  
 115 120 125  
 Ser Met Glu Gln Phe Asn Phe Arg Tyr Ala Glu Lys Thr Asp Phe Glu  
 130 135 140  
 Gln Glu Pro Ser Phe Ala Ser Ile Asp Val Ser Phe Ile Ser Leu Ser  
 145 150 155 160  
 Leu Ile Leu Pro Ala Leu His Arg Val Leu Ala Asp Gln Gly Gln Val  
 165 170 175  
 Val Ala Leu Val Lys Pro Gln Phe Glu Ala Gly Arg Glu Gln Ile Gly  
 180 185 190  
 Lys Asn Gly Ile Ile Arg Asp Ala Lys Val His Gln Asn Val Leu Glu  
 195 200 205  
 Ser Val Thr Ala Met Ala Val Glu Val Gly Phe Ser Val Leu Gly Leu  
 210 215 220  
 Asp Phe Ser Pro Ile Gln Gly Gly His Gly Asn Ile Glu Phe Leu Ala  
 225 230 235 240

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile  
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu  
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCTTAT GAACCTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT	60
TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT	120
CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA	180
TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTCCTT ATGATGCCAT	240
CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT	300
CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAACGGT AAATACTATG TNTACCTTAA	360
GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA	420
ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG	480
ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG	540
TGATGCTTAT ATCGTTCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC	600
AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC	660
TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT	720
GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA	780
ATTGTATGCT AAACCCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC	840
AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAAGCTGTC CCTCATGGTA ACCATTACCA	900
CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATTCCCCT	960
TCGTTATCGT TCAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC	1020
GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAAT CCTCAACCAG CTCCAAGCAA	1080
TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTTCGAAAA GTAGGCGATG GTTATGTCTT	1140
TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AACAGCAGC	1200
AGGCATTGAT AGCAAACCTGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA	1260
AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG	1320

00765274 043204  
 10225260

AATTCACCAA GATTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380  
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440  
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500  
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560  
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620  
 TATGACCCAT AGCCACTGGA TTAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680  
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTTCAGG 1740  
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800  
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860  
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920  
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980  
 CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040  
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100  
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160  
 ACCAGAGTCT CAAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220  
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGGA 2280  
 AATCCAGGAT 2290

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu  
 1 5 10 15

Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala  
 20 25 30

Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala  
 35 40 45

Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His  
 50 55 60

Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile  
 65 70 75 80

Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

85					90					95					
Ser	Asp	Ile	Val	Asn	Glu	Ile	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asn
100								105				110			
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile
115						120						125			
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	Arg	Ser	His	Asn
130					135						140				
His	Asn	Ser	Arg	Ala	Asp	Asn	Ala	Val	Ala	Ala	Ala	Arg	Ala	Gln	Gly
145					150					155	160				
Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile	Ile
				165					170	175					
Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	His
				180					185	190					
Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Glu
195						200					205				
Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser	Ser
210					215					220					
Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn	Leu
225					230					235	240				
Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser
				245					250	255					
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu
				260					265	270					
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala
275						280					285				
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr
290					295					300					
Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu
305					310					315	320				
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro
				325					330	335					
Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro
340						345					350				
Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys
355					360					365					
Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly
370					375					380					
Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala
385					390					395	400				
Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu
				405					410	415					
Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn



430

Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp	Leu	Asp	Asn	
	435						440					445			
Lys	Gly	Arg	Gln	Val	Asp	Phe	Glu	Ala	Leu	Asp	Asn	Leu	Leu	Glu	Arg
	450					455					460				
Leu	Lys	Asp	Val	Xaa	Ser	Asp	Lys	Val	Lys	Leu	Val	Xaa	Asp	Ile	Leu
465					470					475					480
Ala	Phe	Leu	Ala	Pro	Ile	Arg	His	Pro	Glu	Arg	Leu	Gly	Lys	Pro	Asn
				485					490					495	
Ala	Gln	Ile	Thr	Tyr	Thr	Asp	Asp	Glu	Ile	Gln	Val	Ala	Lys	Leu	Ala
			500					505					510		
Gly	Lys	Tyr	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Phe	Asp	Pro	Arg	Asp	Ile
		515					520					525			
Thr	Ser	Asp	Glu	Gly	Asp	Ala	Tyr	Val	Thr	Pro	His	Met	Thr	His	Ser
	530					535					540				
His	Trp	Ile	Lys	Lys	Asp	Ser	Leu	Ser	Glu	Ala	Glu	Arg	Ala	Ala	Ala
545					550					555					560
Gln	Ala	Tyr	Ala	Lys	Glu	Lys	Gly	Leu	Thr	Pro	Pro	Ser	Thr	Asp	His
				565					570					575	
Gln	Asp	Ser	Gly	Asn	Thr	Glu	Ala	Lys	Gly	Ala	Glu	Ala	Ile	Tyr	Asn
			580					585					590		
Arg	Val	Lys	Ala	Ala	Lys	Lys	Val	Pro	Leu	Asp	Arg	Met	Pro	Tyr	Asn
		595					600					605			
Leu	Gln	Tyr	Thr	Val	Glu	Val	Lys	Asn	Gly	Ser	Leu	Ile	Ile	Pro	His
	610					615					620				
Tyr	Asp	His	Tyr	His	Asn	Ile	Lys	Phe	Glu	Trp	Phe	Asp	Glu	Gly	Leu
625					630					635					640
Tyr	Glu	Ala	Pro	Lys	Gly	Tyr	Thr	Leu	Glu	Asp	Leu	Leu	Ala	Thr	Val
				645					650					655	
Lys	Tyr	Tyr	Val	Glu	His	Pro	Asn	Glu	Arg	Pro	His	Ser	Asp	Asn	Gly
			660					665					670		
Phe	Gly	Asn	Ala	Ser	Asp	His	Val	Gln	Arg	Asn	Lys	Asn	Gly	Gln	Ala
		675					680					685			
Asp	Thr	Asn	Gln	Thr	Glu	Lys	Pro	Ser	Glu	Glu	Lys	Pro	Gln	Thr	Glu
	690					695					700				
Lys	Pro	Glu	Glu	Glu	Thr	Pro	Arg	Glu	Glu	Lys	Pro	Gln	Ser	Glu	Lys
705					710					715					720
Pro	Glu	Ser	Pro	Lys	Pro	Thr	Glu	Glu	Pro	Glu	Glu	Ser	Pro	Glu	Glu
				725					730					735	
Ser	Glu	Glu	Pro	Gln	Val	Glu	Thr	Glu	Lys	Val	Glu	Glu	Lys	Leu	Arg
			740					745					750		
Glu	Ala	Glu	Asp	Leu	Leu	Gly	Lys	Ile	Gln	Asp					

755

760

## (2) INFORMATION FOR SEQ ID NO: 67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA 60  
 AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAACCTGT 120  
 ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA 180  
 AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA 240  
 TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT 300  
 TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG 352

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile  
 1 5 10 15  
 Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser  
 20 25 30  
 Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys  
 35 40 45  
 Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn  
 50 55 60  
 Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp  
 65 70 75 80  
 Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val  
 85 90 95  
 Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr  
 100 105 110  
 Asn Asn Pro Asn Lys  
 115

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG 60

TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA 120

AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC 180

GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA 240

AAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA 300

ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT 360

TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC 420

TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT 480

TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT 540

AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA 600

GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGA GCAGAAGACA AGTATGGTCC 660

TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA 720

TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT 780

ACCTTGAAA AATGGTGTTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA 840

GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG 900

TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA 960

GAGTGCATAT GGGAAGTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCTGG 1020

TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA 1080

TCAATGGAAG AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTTCTGCTAA 1140

AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT 1200

TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC 1260

AGGATGGCTT CAATATATGG GGCAATGGTA TTACTTTGCT CCATCAGGGG AA 1312

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00765274 0122004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn	Val	Gln	Ala	Gln	Glu	Ser	Ser	Gly	Asn	Lys	Ile	His	Phe	Ile	Asn
1				5					10						15
Val	Gln	Glu	Gly	Gly	Ser	Asp	Ala	Ile	Ile	Leu	Glu	Ser	Asn	Gly	His
			20					25					30		
Phe	Ala	Met	Val	Asp	Thr	Gly	Glu	Asp	Tyr	Asp	Phe	Pro	Asp	Gly	Ser
		35					40					45			
Asp	Ser	Arg	Tyr	Pro	Trp	Arg	Glu	Gly	Ile	Glu	Thr	Ser	Tyr	Lys	His
	50					55					60				
Val	Leu	Thr	Asp	Arg	Val	Phe	Arg	Arg	Leu	Lys	Glu	Leu	Gly	Val	Gln
65					70					75					80
Lys	Leu	Asp	Phe	Ile	Leu	Val	Thr	His	Thr	His	Ser	Asp	His	Ile	Gly
				85					90					95	
Asn	Val	Asp	Glu	Leu	Leu	Ser	Thr	Tyr	Pro	Val	Asp	Arg	Val	Tyr	Leu
			100					105					110		
Lys	Lys	Tyr	Ser	Asp	Ser	Arg	Ile	Thr	Asn	Ser	Glu	Arg	Leu	Trp	Asp
		115					120					125			
Asn	Leu	Tyr	Gly	Tyr	Asp	Lys	Val	Leu	Gln	Thr	Ala	Ala	Glu	Lys	Gly
		130				135					140				
Val	Ser	Val	Ile	Gln	Asn	Ile	Thr	Gln	Gly	Asp	Ala	His	Phe	Gln	Phe
145					150					155					160
Gly	Asp	Met	Asp	Ile	Gln	Leu	Tyr	Asn	Tyr	Glu	Asn	Glu	Thr	Asp	Ser
				165					170					175	
Ser	Gly	Glu	Leu	Lys	Lys	Ile	Trp	Asp	Asp	Asn	Ser	Asn	Ser	Leu	Ile
			180					185					190		
Ser	Val	Val	Lys	Val	Asn	Gly	Lys	Lys	Ile	Tyr	Leu	Gly	Gly	Asp	Leu
		195					200					205			
Asp	Asn	Val	His	Gly	Ala	Glu	Asp	Lys	Tyr	Gly	Pro	Leu	Ile	Gly	Lys
		210				215					220				
Val	Asp	Leu	Met	Lys	Phe	Asn	His	His	His	Asp	Thr	Asn	Lys	Ser	Asn
225					230					235					240
Thr	Lys	Asp	Phe	Ile	Lys	Asn	Leu	Ser	Pro	Ser	Leu	Ile	Val	Gln	Thr
				245					250					255	
Ser	Asp	Ser	Leu	Pro	Trp	Lys	Asn	Gly	Val	Asp	Ser	Glu	Tyr	Val	Asn
			260					265					270		
Trp	Leu	Lys	Glu	Arg	Gly	Ile	Glu	Arg	Ile	Asn	Ala	Ala	Ser	Lys	Asp
		275					280					285			
Tyr	Asp	Ala	Thr	Val	Phe	Asp	Ile	Arg	Lys	Asp	Gly	Phe	Val	Asn	Ile
		290				295					300				

Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys  
305 310 315 320

Ser-Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu  
325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn  
340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His  
355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys  
370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile  
385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly  
405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe  
420 425 430

Ala Pro Ser Gly Glu  
435

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780  
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT 840  
 CAAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900  
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG 960  
 ACGTACTAAA CAATTCGGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020  
 AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080  
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140  
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200  
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260  
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320  
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380  
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440  
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500  
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAAATG GAACTAGCCA 1560  
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA 1620  
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680  
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740  
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTC GAAACGAATC 1800  
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe  
 1 5 10 15  
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser  
 20 25 30  
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu  
 35 40 45  
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala  
 50 55 60

Glu	Phe	Lys	Asn	Leu	Ile	Asn	Glu	Ile	His	Lys	Arg	Gly	Met	Gly	Ala	65	70	75	80
Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Lys	Val	Asp	Leu	Phe	Glu	85	90	95	
Asp	Leu	Glu	Pro	Asn	Tyr	Tyr	His	Phe	Met	Asp	Ala	Asp	Gly	Thr	Pro	100	105	110	
Arg	Thr	Ser	Phe	Gly	Gly	Gly	Arg	Leu	Gly	Thr	Thr	His	His	Met	Thr	115	120	125	
Lys	Arg	Leu	Leu	Ile	Asp	Ser	Ile	Lys	Tyr	Leu	Val	Asp	Thr	Tyr	Lys	130	135	140	
Val	Asp	Gly	Phe	Arg	Phe	Asp	Met	Met	Gly	Asp	His	Asp	Ala	Ala	Ser	145	150	155	160
Ile	Glu	Glu	Ala	Tyr	Lys	Ala	Ala	Arg	Ala	Leu	Asn	Pro	Asn	Leu	Ile	165	170	175	
Met	Leu	Gly	Glu	Gly	Trp	Arg	Thr	Tyr	Ala	Gly	Asp	Glu	Asn	Met	Pro	180	185	190	
Thr	Lys	Ala	Ala	Asp	Gln	Asp	Trp	Met	Lys	His	Thr	Asp	Thr	Val	Ala	195	200	205	
Val	Phe	Ser	Asp	Asp	Ile	Arg	Asn	Asn	Leu	Lys	Ser	Gly	Tyr	Pro	Asn	210	215	220	
Glu	Gly	Gln	Pro	Ala	Phe	Ile	Thr	Gly	Gly	Lys	Arg	Asp	Val	Asn	Thr	225	230	235	240
Ile	Phe	Lys	Asn	Leu	Ile	Ala	Gln	Pro	Thr	Asn	Phe	Glu	Ala	Asp	Ser	245	250	255	
Pro	Gly	Asp	Val	Ile	Gln	Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu	260	265	270	
Phe	Asp	Ile	Ile	Ala	Gln	Ser	Ile	Lys	Lys	Asp	Pro	Ser	Lys	Ala	Glu	275	280	285	
Asn	Tyr	Ala	Glu	Ile	His	Arg	Arg	Leu	Arg	Leu	Gly	Asn	Leu	Met	Val	290	295	300	
Leu	Thr	Ala	Gln	Gly	Thr	Pro	Phe	Ile	His	Ser	Gly	Gln	Glu	Tyr	Gly	305	310	315	320
Arg	Thr	Lys	Gln	Phe	Arg	Asp	Pro	Ala	Tyr	Lys	Thr	Pro	Val	Ala	Glu	325	330	335	
Asp	Lys	Val	Pro	Asn	Lys	Ser	His	Leu	Leu	Arg	Asp	Lys	Asp	Gly	Asn	340	345	350	
Pro	Phe	Asp	Tyr	Pro	Tyr	Phe	Ile	His	Asp	Ser	Tyr	Asp	Ser	Ser	Asp	355	360	365	
Ala	Val	Asn	Lys	Phe	Asp	Trp	Thr	Lys	Ala	Thr	Asp	Gly	Lys	Ala	Tyr	370	375	380	
Pro	Glu	Asn	Val	Lys	Ser	Arg	Asp	Tyr	Met	Lys	Gly	Leu	Ile	Ala	Leu	385	390	395	400

Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys  
405 410 415

Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys  
420 425 430

Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile  
435 440 445

Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu  
450 455 460

Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu  
465 470 475 480

Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp  
485 490 495

Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg  
500 505 510

Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro  
515 520 525

Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro  
530 535 540

Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro  
545 550 555 560

Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala  
565 570 575

Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val  
580 585 590

Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn  
595 600 605

Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu  
610 615

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300



AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360  
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420  
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480  
 AGTACAGCAA GGTGCGCTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540  
 TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600  
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660  
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGCTA 720  
 CTACTTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780  
 GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840  
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900  
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960  
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020  
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080  
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140  
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200  
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260  
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320  
 TTTCAAAGAT TTAACAGAGG CTACAAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380  
 TTTGCTAAAC ATTAACAATA GCCTTTTGGG GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440  
 AGAACATTAC CATATCAATG CTCTTTATCT CTTGCCCCAT AGTGCCCTAG AAAGTAACTG 1500  
 GGGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560  
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620  
 CAAGTGGAAT AAGGAAAATT ATATCGATAG GGGAAGAACT TTCCTTGGA ACAAGGCTTC 1680  
 TGGTATGAAT GTGGAATATG CTTAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740  
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Tyr	Tyr	Gln	Val	Val	Phe	Val	His	Ala	Asn	Val	Tyr	Asp	Ser	Leu	Cys
					325				330					335	

Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys  
 340 345 350  
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu  
 355 360 365  
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys  
 370 375 380  
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr  
 385 390 395 400  
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met  
 405 410 415  
 Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly  
 420 425 430  
 Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr  
 435 440 445  
 Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile  
 450 455 460  
 Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu  
 465 470 475 480  
 Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu  
 485 490 495  
 Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe  
 500 505 510  
 Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr  
 515 520 525  
 Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys  
 530 535 540  
 Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser  
 545 550 555 560  
 Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile  
 565 570 575  
 Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp  
 580 585 590

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA

CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA 120  
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC 180  
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC 240  
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT 300  
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTTG CTACTAAATA 360  
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG 420  
GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG 480  
TACTTTAAGT CAAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA 540  
AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA 600  
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660  
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT 720  
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780  
ATCATCTATT CTTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840  
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900  
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960  
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020  
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080  
CAATGATAAT GGTGAATGGG TGCCT 1105

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile  
1 5 10 15  
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr  
20 25 30  
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr  
35 40 45  
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp  
50 55 60  
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro  
65 70 75 80

Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala  
 85 90 95  
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val  
 100 105 110  
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala  
 115 120 125  
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr  
 130 135 140  
 Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser  
 145 150 155 160  
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg  
 165 170 175  
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr  
 180 185 190  
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly  
 195 200 205  
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg  
 210 215 220  
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met  
 225 230 235 240  
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val  
 245 250 255  
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser  
 260 265 270  
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro  
 275 280 285  
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr  
 290 295 300  
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr  
 305 310 315 320  
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val  
 325 330 335  
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn  
 340 345 350  
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 661 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AACCTTTAT GACGGGTGAA AATTTTATC TCCAACATTA 60  
 TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120  
 ACCTAATGCT CAGGCTGTTC ACTTGGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT 180  
 TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240  
 GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300  
 TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360  
 GAAGAAATGG AAGGATGGAC TT'TGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420  
 TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAG AGAAATTCTG ATGGCAGTCC 480  
 TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTAT CTCGTTGAAA TGAACATAC 540  
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600  
 TATGGGTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660  
 C 661

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr  
 1                      5                      10                      15  
 Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His  
 20                      25                      30  
 Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu  
 35                      40                      45  
 Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg  
 50                      55                      60  
 Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly  
 65                      70                      75                      80  
 His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met  
 85                      90                      95  
 Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly  
 100                      105                      110  
 Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
165	170	175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
180	185	190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
195	200	205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
210	215	220

## (2) INFORMATION FOR SEQ ID NO: 79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN	60
TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGAAAA	180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTG ACTACAAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTCG CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCGC	840
TTCTCAGCTA AACCAGTTTT ACAAGATCA TCGCTGTCTG TGGGAAATG ATACCAGCTA	900
TGATGGTATT GAAATCATTG ATGCGGATAA TCGAGACCAG AGTGTCTTTT CCTTTATTCTG	960

976

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu  
245 250 255



Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met  
260 265 270

Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys  
275 280 285

Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu  
290 295 300

Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg  
305 310 315 320

Lys Gly Lys Lys Gly  
325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA	60
AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG	120
GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA	180
AGCCGTA ACT CCAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT	240
AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA	300
TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT	360
TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA	420
AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC	480
ACAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAA ACT	540
AGATGAAAAA GACCTCAAGA AAAATGTTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC	600
TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC	660
ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC	720
AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC	780
TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA	840
ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC	900
GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC	960
TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT	1020
AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC	1080

CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140  
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA 1200  
 ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260  
 AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAAGTCCAT 1320  
 CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380  
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440  
 ACGTTTCCTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500  
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAACAAC CCTGCTATCT TCATGTGGTC 1560  
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTAAACG 1620  
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680  
 ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740  
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800  
 GATTTATGGA TCAGAAACAT CTTACAGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860  
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920  
 TGATCGTGTG GGTGAGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980  
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040  
 GCACAACCAA AATCAAATC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100  
 CATTCACAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys  
 1 5 10 15  
 Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu  
 20 25 30  
 Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser  
 35 40 45  
 Thr Glu Ala Ile Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro  
 50 55 60  
 Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

65					70					75					80				
Glu	Ser	Gln	Ala	Ser	Asn	Gln	Glu	Lys	Pro	Leu	Lys	Glu	Asp	Ala	Lys				
				85					90					95					
Ala	Val	Thr	Asn	Glu	Glu	Val	Asn	Gln	Met	Ile	Glu	Asp	Arg	Lys	Val				
			100					105					110						
Asp	Phe	Asn	Gln	Asn	Trp	Tyr	Phe	Lys	Leu	Asn	Ala	Asn	Ser	Lys	Glu				
		115					120					125							
Ala	Ile	Lys	Pro	Asp	Ala	Asp	Val	Ser	Thr	Trp	Lys	Lys	Leu	Asp	Leu				
		130				135					140								
Pro	Tyr	Asp	Trp	Ser	Ile	Phe	Asn	Asp	Phe	Asp	His	Glu	Ser	Pro	Ala				
145					150					155					160				
Gln	Asn	Glu	Gly	Gly	Gln	Leu	Asn	Gly	Gly	Glu	Ala	Trp	Tyr	Arg	Lys				
				165					170					175					
Thr	Phe	Lys	Leu	Asp	Glu	Lys	Asp	Leu	Lys	Lys	Asn	Val	Arg	Leu	Thr				
			180					185					190						
Phe	Asp	Gly	Val	Tyr	Met	Asp	Ser	Gln	Val	Tyr	Val	Asn	Gly	Gln	Leu				
		195					200					205							
Val	Gly	His	Tyr	Pro	Asn	Gly	Tyr	Asn	Gln	Phe	Ser	Tyr	Asp	Ile	Thr				
	210					215					220								
Lys	Tyr	Leu	Gln	Lys	Asp	Gly	Arg	Glu	Asn	Val	Ile	Ala	Val	His	Ala				
225					230					235					240				
Val	Asn	Lys	Gln	Pro	Ser	Ser	Arg	Trp	Tyr	Ser	Gly	Ser	Gly	Ile	Tyr				
				245					250					255					
Arg	Asp	Val	Thr	Leu	Gln	Val	Thr	Asp	Lys	Val	His	Val	Glu	Lys	Asn				
			260					265					270						
Gly	Thr	Thr	Ile	Leu	Thr	Pro	Lys	Leu	Glu	Glu	Gln	Gln	His	Gly	Lys				
		275					280					285							
Val	Glu	Thr	His	Val	Thr	Ser	Lys	Ile	Val	Asn	Thr	Asp	Asp	Lys	Asp				
		290				295					300								
His	Glu	Leu	Val	Ala	Glu	Tyr	Gln	Ile	Val	Glu	Arg	Gly	Gly	His	Ala				
305					310					315					320				
Val	Thr	Gly	Leu	Val	Arg	Thr	Ala	Ser	Arg	Thr	Leu	Lys	Ala	His	Glu				
				325					330					335					
Ser	Thr	Ser	Leu	Asp	Ala	Ile	Leu	Glu	Val	Glu	Arg	Pro	Lys	Leu	Trp				
			340					345				350							
Thr	Val	Leu	Asn	Asp	Lys	Pro	Ala	Leu	Tyr	Glu	Leu	Ile	Thr	Arg	Val				
			355				360					365							
Tyr	Arg	Asp	Gly	Gln	Leu	Val	Asp	Ala	Lys	Lys	Asp	Leu	Phe	Gly	Tyr				
	370					375					380								
Arg	Tyr	Tyr	His	Trp	Thr	Pro	Asn	Glu	Gly	Phe	Ser	Leu	Asn	Gly	Glu				
385					390					395					400				
Arg	Ile	Lys	Phe	His	Gly	Val	Ser	Leu	His	His	Asp								

405

410

415

Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met  
 420 425 430  
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser  
 435 440 445  
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu  
 450 455 460  
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly  
 465 470 475 480  
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu  
 485 490 495  
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn  
 500 505 510  
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala  
 515 520 525  
 Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val  
 530 535 540  
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys  
 545 550 555 560  
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu  
 565 570 575  
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu  
 580 585 590  
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser  
 595 600 605  
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys  
 610 615 620  
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn  
 625 630 635 640  
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp  
 645 650 655  
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp  
 660 665 670  
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val  
 675 680 685  
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His  
 690 695 700  
 Asp Phe Tyr Leu Tyr Gln Ser  
 705 710

(2) INFORMATION FOR SEQ ID NO: 83:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAGTCTG AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACTT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGACAC AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAATTT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680

GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA 1740  
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800  
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860  
 CACTTGGCAA GCTATTCCGA AAGAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920  
 TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980  
 AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040  
 TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTCTG 2100  
 TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA 2160  
 ATTAACA 2167

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr  
 1 5 10 15  
 Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His  
 20 25 30  
 Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val  
 35 40 45  
 Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser  
 50 55 60  
 Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe  
 65 70 75 80  
 Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn  
 85 90 95  
 Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr  
 100 105 110  
 Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp  
 115 120 125  
 Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu  
 130 135 140  
 Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr  
 145 150 155 160  
 Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu

165										170				175					
Val	Arg	Phe	Gln	Leu	His	Gly	Gln	Gly	Gln	Leu	Val	Gly	Val	Asp	Asn				
			180						185					190					
Gly	Glu	Gln	Ala	Ser	Arg	Glu	Arg	Tyr	Lys	Ala	Gln	Ala	Asp	Gly	Ser				
			195					200					205						
Trp	Ile	Arg	Lys	Ala	Phe	Asn	Gly	Lys	Gly	Val	Ala	Ile	Val	Lys	Ser				
			210				215						220						
Thr	Glu	Gln	Ala	Gly	Lys	Phe	Thr	Leu	Thr	Ala	His	Ser	Asp	Leu	Leu				
						230					235				240				
Lys	Ser	Asn	Gln	Val	Thr	Val	Phe	Thr	Gly	Lys	Lys	Glu	Gly	Gln	Glu				
					245					250					255				
Lys	Thr	Val	Leu	Gly	Thr	Glu	Val	Pro	Lys	Val	Gln	Thr	Ile	Ile	Gly				
					260				265					270					
Glu	Ala	Pro	Glu	Met	Pro	Thr	Thr	Val	Pro	Phe	Val	Tyr	Ser	Asp	Gly				
								280					285						
Ser	Arg	Ala	Glu	Arg	Pro	Val	Thr	Trp	Ser	Ser	Val	Asp	Val	Ser	Lys				
							295					300							
Pro	Gly	Ile	Val	Thr	Val	Lys	Gly	Met	Ala	Asp	Gly	Arg	Glu	Val	Glu				
						310				315					320				
Ala	Arg	Val	Glu	Val	Ile	Ala	Leu	Lys	Ser	Glu	Leu	Pro	Val	Val	Lys				
						325				330					335				
Arg	Ile	Ala	Pro	Asn	Thr	Asp	Leu	Asn	Ser	Val	Asp	Lys	Ser	Val	Ser				
						340			345					350					
Tyr	Val	Leu	Ile	Asp	Gly	Ser	Val	Glu	Glu	Tyr	Glu	Val	Asp	Lys	Trp				
							360						365						
Glu	Ile	Ala	Glu	Glu	Asp	Lys	Ala	Lys	Leu	Ala	Ile	Pro	Gly	Ser	Arg				
						375						380							
Ile	Gln	Ala	Thr	Gly	Tyr	Leu	Glu	Gly	Gln	Pro	Ile	His	Ala	Thr	Leu				
						390				395					400				
Val	Val	Glu	Glu	Gly	Asn	Pro	Ala	Ala	Pro	Ala	Val	Pro	Thr	Val	Thr				
						405				410					415				
Val	Gly	Gly	Glu	Ala	Val	Thr	Gly	Leu	Thr	Ser	Gln	Lys	Pro	Met	Gln				
						420			425				430						
Tyr	Arg	Thr	Leu	Ala	Tyr	Gly	Ala	Lys	Leu	Pro	Glu	Val	Thr	Ala	Ser				
							440						445						
Ala	Lys	Asn	Ala	Ala	Val	Thr	Val	Leu	Gln	Ala	Ser	Ala	Ala	Asn	Gly				
							455					460							

202

500

505

510

Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu  
515 520 525

Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala  
530 535 540

Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu  
545 550 555 560

Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln  
565 570 575

Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val  
580 585 590

Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val  
595 600 605

Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala  
610 615 620

Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly  
625 630 635 640

Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu  
645 650 655

Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu  
660 665 670

Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His  
675 680 685

Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr  
690 695 700

Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln  
705 710 715 720

Leu Thr

## (2) INFORMATION FOR SEQ ID NO: 85:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTCTGCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC	120
TCAAAGTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240



CTACAATAAC	CAACCAGCCA	ATCGTTGGAC	AAACTGGAAT	CGTACTAATC	CAGAAGCTTC	300
AGTCGGTGTT	CTGTTTGGAG	ATTCAGGTAT	CTTGAGCAAA	CGCTCCGTTG	ATAATCTAAG	360
TGTCGGATTC	CATGAAGACC	ATGGAGTTGG	TGTACCGAAG	TCTTATGTGA	TTGAGTATTA	420
TGTTGGTAAG	ACTGTCCCAA	CAGCTCCTAA	AAACCCTAGT	TTTGTTGGTA	ATGAGGACCA	480
TGTCTTTAAT	GATTCTGCCA	ACTGGAAACC	AGTTACTAAT	CTAAAAGCCC	CTGCTCAACT	540
CAAGGCTGGA	GAAATGAACC	ACTTTAGCTT	TGATAAAGTT	GAAACCTATG	CTGTTCGTAT	600
TCGCATGGTT	AAAGCAGATA	ACAAGCGTGG	AACGTCTATC	ACAGAGGTAC	AAATCTTTGC	660
GAAACAAGTT	GCGGCAGCCA	AGCAAGGACA	AACAAGAATC	CAAGTTGACG	GCAAAGACTT	720
AGCAAAC TTC	AACCCTGATT	TGACAGACTA	CTACCTTGAG	TCTGTAGATG	GAAAAGTTCC	780
GGCAGTCACA	GCAAGTGTTA	GCAACAATGG	TCTCGCTACC	GTCGTTCCAA	GCGTTCGTGA	840
AGGTGAGCCA	GTTTCGTGTCA	TCGCGAAAGC	TGAAAATGGC	GACATCTTAG	GAGAATACCG	900
TCTGCACTTC	ACTAAGGATA	AGAGCTTACT	TTCTCATAAA	CCAGTTGCTG	CGGTAAACA	960
AGCTCGCTTG	CTACAAGTAG	GTCAAGCACT	TGAATTGCCG	ACTAAGGTTT	CAGTTTACTT	1020
CACAGGTAAA	GACGGCTACG	AAACAAAAGA	CCTGACAGTT	GAATGGGAAG	AAGTTCCAGC	1080
GGAAAATCTG	ACAAAAGCAG	GTCAATTTAC	TGTTGAGGGC	CGTGTCCTTG	G TAGTAACCT	1140
TGTTGCTGAG	ATCACTGTAC	GAGTGACAGA	CAAAC TTGGT	GAGACTCTTT	CAGATAACCC	1200
TAAC TATGAT	GAAAACAGTA	ACCAGGCCTT	TGCTTCAGCA	ACCAATGATA	TTGACAAAAA	1260
CTCTCATGAC	CGCGTTGACT	ATCTCAATGA	CGGAGATCAT	TCAGAAAATC	GTCGTTGGAC	1320
AAACTGGTCA	CCAACACCAT	CTTCTAATCC	AGAAGTATCA	GCGGGTGTGA	TTTTCCGTGA	1380
AAATGGTAAG	ATTGTAGAAC	GGACTGTTAC	ACAAGGAAAA	G TTCAGTTCT	TTGCAGATAG	1440
TGGTACGGAT	GCACCATCTA	AACTCGTTTT	AGAACGCTAT	GTCGGTCCAG	AGTTTGAAGT	1500
GCCAACCTAC	TATTCAAAC T	ACCAAGCCTA	CGACGCAGAC	CATCCATTCA	ACAATCCAGA	1560
AAATTGGGAA	GCTGTTCC TT	ATCGTGCGGA	TAAAGACATT	GCAGCTGGTG	ATGAAATCAA	1620
CGTAACATTT	AAAGCTATCA	AAGCCAAAGC	TATGAGATGG	CGTATGGAGC	GTAAAGCAGA	1680
TAAGAGCGGT	GTTGCGATGA	TTGAGATGAC	CTTCCTTGCA	CCAAGTGAAT	TGCCTCAAGA	1740
AAGCACTCAA	TCAAAGATTC	TTGTAGATGG	AAAAGAACTT	GCTGATTTCTG	CTGAAAATCG	1800
.TCAAGACTAT	CAAATTACCT	ATAAAGGTCA	ACGGCCAAAA	GTCTCAGTTG	AAGAAAACAA	1860
TCAAGTAGCT	TCAACTGTGG	TAGATAGTGG	AGAAGATAGC	TTTCCAGTAC	TTGTTGCGCT	1920
CGTTTTCAGAA	AGTGGA AAAC	AAGTCAAGGA	ATACCGTATC	C ACTTGACTA	AGGAAAAACC	1980
AGTTTCTGAG	AAGACAGTTG	CTGCTGTACA	AGAAGATCTT	CCAAAAATCG	AATTTGTTGA	2040
AAAAGATTTG	GCATACAAGA	CAGTTGAGAA	AAAAGATTCA	ACACTGTATC	TAGGTGAAAC	2100

TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160  
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220  
 GGTGGAACC AAACCAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTCAG AAAAAGCAGA 2280  
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAA~~ACT~~AAT AAAGCCCAG 2329

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala	Lys	Val	Ala	Trp	Asp	Ala	Ile	Arg	Pro	Glu	Gln	Tyr	Ala	Lys	Glu	1	5	10	15
Gly	Val	Phe	Thr	Val	Asn	Gly	Arg	Leu	Glu	Gly	Thr	Gln	Leu	Thr	Thr	20	25	30	
Lys	Leu	His	Val	Arg	Val	Ser	Ala	Gln	Thr	Glu	Gln	Gly	Ala	Asn	Ile	35	40	45	
Ser	Asp	Gln	Trp	Thr	Gly	Ser	Glu	Leu	Pro	Leu	Ala	Phe	Ala	Ser	Asp	50	55	60	
Ser	Asn	Pro	Ser	Asp	Pro	Val	Ser	Asn	Val	Asn	Asp	Lys	Leu	Ile	Ser	65	70	75	80
Tyr	Asn	Asn	Gln	Pro	Ala	Asn	Arg	Trp	Thr	Asn	Trp	Asn	Arg	Thr	Asn	85	90	95	
Pro	Glu	Ala	Ser	Val	Gly	Val	Leu	Phe	Gly	Asp	Ser	Gly	Ile	Leu	Ser	100	105	110	
Lys	Arg	Ser	Val	Asp	Asn	Leu	Ser	Val	Gly	Phe	His	Glu	Asp	His	Gly	115	120	125	
Val	Gly	Val	Pro	Lys	Ser	Tyr	Val	Ile	Glu	Tyr	Tyr	Val	Gly	Lys	Thr	130	135	140	
Val	Pro	Thr	Ala	Pro	Lys	Asn	Pro	Ser	Phe	Val	Gly	Asn	Glu	Asp	His	145	150	155	160
Val	Phe	Asn	Asp	Ser	Ala	Asn	Trp	Lys	Pro	Val	Thr	Asn	Leu	Lys	Ala	165	170	175	
Pro	Ala	Gln	Leu	Lys	Ala	Gly	Glu	Met	Asn	His	Phe	Ser	Phe	Asp	Lys	180	185	190	
Val	Glu	Thr	Tyr	Ala	Val	Arg	Ile	Arg	Met	Val	Lys	Ala	Asp	Asn	Lys	195	200	205	
Arg	Gly	Thr	Ser	Ile	Thr	Glu	Val	Gln	Ile	Phe	Ala	Lys	Gln	Val	Ala	210	215	220	

0076324 04200

Ala Ala Lys Gln Gly Gln Thr Arg Ile Gln Val Asp Gly Lys Asp Leu  
 225 230 235 240  
 Ala Asn Phe Asn Pro Asp Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp  
 245 250 255  
 Gly Lys Val Pro Ala Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala  
 260 265 270  
 Thr Val Val Pro Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala  
 275 280 285  
 Lys Ala Glu Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr  
 290 295 300  
 Lys Asp Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln  
 305 310 315 320  
 Ala Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val  
 325 330 335  
 Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu Thr  
 340 345 350  
 Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala Gly Gln  
 355 360 365  
 Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val Ala Glu Ile  
 370 375 380  
 Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu Ser Asp Asn Pro  
 385 390 395 400  
 Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala Ser Ala Thr Asn Asp  
 405 410 415  
 Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly Asp  
 420 425 430  
 His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser Ser  
 435 440 445  
 Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys Ile  
 450 455 460  
 Val Glu Arg Thr Val Thr Gln Gly Lys Val Gln Phe Phe Ala Asp Ser  
 465 470 475 480  
 Gly Thr Asp Ala Pro Ser Lys Leu Val Leu Glu Arg Tyr Val Gly Pro  
 485 490 495  
 Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala  
 500 505 510  
 Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg  
 515 520 525  
 Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys  
 530 535 540  
 Ala Ile Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp  
 545 550 555 560

0076527-042204  
 102210-1255160



- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1           5           10           15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
          20           25           30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
          35           40

```

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA      60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAATAAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT       775

```

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 258 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

09763414394

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn  
 1 5 10 15  
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr  
 20 25 30  
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp  
 35 40 45  
 Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro  
 50 55 60  
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu  
 65 70 75 80  
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu  
 85 90 95  
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp  
 100 105 110  
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu  
 115 120 125  
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp  
 130 135 140  
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln  
 145 150 155 160  
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr  
 165 170 175  
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala  
 180 185 190  
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys  
 195 200 205  
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys  
 210 215 220  
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys  
 225 230 235 240  
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr  
 245 250 255  
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

GGATGCTCAA GAAACTGCGG GAGTTCAC TA AATATGTG GCAGATTCAG AGCTATCATC      60
AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC      120
TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG      180
AAGCAAGAAT GAGAGGCAA                                     199

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser
1           5           10           15
Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr
20           25           30
Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn
35           40           45
Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu
50           55           60
Arg Gln
65

```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG      60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC      120
TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT      180
AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT      240

```

TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300  
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360  
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420  
 AAAAAGTGTGA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480  
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAAT 540  
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600  
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660  
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720  
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAAATGA 780  
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val  
 1 5 10 15  
 Ser Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys  
 20 25 30  
 Gly Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys  
 35 40 45  
 Glu Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu  
 50 55 60  
 Glu Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile  
 65 70 75 80  
 Gln Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn  
 85 90 95  
 Ser Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val  
 100 105 110  
 Ser Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys  
 115 120 125  
 Pro Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu  
 130 135 140  
 Glu Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn  
 145 150 155 160



Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn  
 165 170 175  
 Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro  
 180 185 190  
 Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn  
 195 200 205  
 Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn  
 210 215 220  
 Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val  
 225 230 235 240  
 Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys  
 245 250 255  
 Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys  
 260 265 270  
 Thr Leu Glu Leu Arg Asn  
 275

## (2) INFORMATION FOR SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA	60
ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA	120
TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC	180
AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC	240
GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC	300
TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG	360
CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG	420
TTACAAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC	480
TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCGCT	540
TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGA GCAGAAAAAC AAGCAGCTCT	600
CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT	660
GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT	709

## (2) INFORMATION FOR SEQ ID NO: 96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Asn	Gln	Leu	Val	Ala	Gln	Asp	Pro	Lys	Ala	Gln	Asp	Ser	Thr	Lys	Leu	1	5	10	15
Thr	Ala	Glu	Lys	Ser	Thr	Val	Lys	Ala	Pro	Ala	Gln	Arg	Val	Asp	Val	20	25	30	
Lys	Asp	Ile	Thr	His	Leu	Thr	Asp	Glu	Glu	Lys	Val	Lys	Val	Ala	Ile	35	40	45	
Leu	Gln	Ala	Asn	Gly	Ser	Ala	Leu	Asp	Gly	Ala	Thr	Ile	Asn	Val	Ala	50	55	60	
Gly	Asp	Gly	Thr	Ala	Thr	Ile	Thr	Phe	Pro	Asp	Gly	Ser	Val	Val	Thr	65	70	75	80
Ile	Leu	Gly	Lys	Asp	Thr	Val	Gln	Gln	Ser	Ala	Lys	Gly	Glu	Ser	Val	85	90	95	
Thr	Gln	Glu	Ala	Thr	Pro	Glu	Tyr	Lys	Leu	Glu	Asn	Thr	Pro	Gly	Gly	100	105	110	
Asp	Lys	Gly	Gly	Asn	Thr	Gly	Ser	Ser	Asp	Ala	Asn	Ala	Asn	Glu	Gly	115	120	125	
Gly	Gly	Ser	Gln	Ala	Gly	Gly	Ser	Ala	His	Thr	Gly	Ser	Gln	Asn	Ser	130	135	140	
Ala	Gln	Ser	Gln	Ala	Ser	Lys	Gln	Leu	Ala	Thr	Glu	Lys	Glu	Ser	Ala	145	150	155	160
Lys	Asn	Ala	Ile	Glu	Lys	Ala	Ala	Lys	Asp	Lys	Gln	Asp	Glu	Ile	Lys	165	170	175	
Gly	Ala	Pro	Leu	Ser	Asp	Lys	Glu	Lys	Ala	Glu	Leu	Leu	Ala	Arg	Val	180	185	190	
Glu	Ala	Glu	Lys	Gln	Ala	Ala	Leu	Lys	Glu	Ile	Glu	Asn	Ala	Lys	Thr	195	200	205	
Met	Glu	Asp	Val	Lys	Glu	Ala	Glu	Thr	Ile	Gly	Val	Gln	Ala	Ile	Ala	210	215	220	
Met	Val	Thr	Val	Pro	Lys	Arg	Pro	Val	Ala	Pro	Asn					225	230	235	

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA	GCTTCAGGAA	CGATTGAGGT	GATTTACACGA	GAAATGGCT	CTGGGACACG	60
GGGTGCCTTC	ACAGAAATCA	CAGGGATTCT	CAAAAAAGAC	GGTGATAAAA	AAATTGACAA	120
CACTGCCAAA	ACAGCTGTGA	TTCAAAATAG	TACAGAAGGT	GTTCTCTCAG	CAGTTCAAGG	180
GAATGCTAAT	GCTATCGGCT	ACATCTCCTT	GGGATCTTTA	ACGAAATCTG	TCAAGGCTTT	240
AGAGATTGAT	GGTGTCAAGG	CTAGTCGAGA	CACAGTTTTA	GATGGTGAAT	ACCTCTTTCA	300
ACGTCCCTTC	AACATTGTTT	GGTCTTCTAA	TCTTTCCAAG	CTAGGTCAAG	ATTTTATCAG	360
CTTTATCCAC	TCCAAACAAG	GTCAACAAGT	GGTCACAGAT	AATAAATTTA	TTGAAGCTAA	420
AACCGAAACC	ACGGAATATA	CAAGCCAACA	CTTATCAGGC	AAGTTGTCTG	TTGTAGGTTT	480
CACTTCAGTA	TCTTCTTTAA	TGGAAAAATT	AGCAGAAGCT	TATAAAAAAG	AAAATCCAGA	540
AGTTACGATT	GATATTACCT	CTAATGGGTC	TTCAGCAGGT	ATTACCGCTG	TTAAGGAGAA	600
AACCGCTGAT	ATTGGTATGG	TTTCTAGGGA	ATTAACCTCT	GAAGAAGGTA	AGAGTCTCAC	660
CCATGATGCT	ATTGCTTTAG	ACGGTATTGC	TGTTGTGGTC	AATAATGACA	ATAAGGCAAG	720
CCAAGTCAGT	ATGGCTGAAC	TTGCAGACGT	TTTTAGTGGC	AAATTAACCA	CCTGGGACAA	780
GATTAAA						787

(2) INFORMATION FOR SEO ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:98:

Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly
1				5					10						15
Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys
			20					25					30		
Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln
		35					40					45			
Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala
	50					55					60				
Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu
65					70					75					80
Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu
				85					90					95	

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser  
 100 105 110  
 Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln  
 115 120 125  
 Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr  
 130 135 140  
 Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser  
 145 150 155 160  
 Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys  
 165 170 175  
 Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala  
 180 185 190  
 Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser  
 195 200 205  
 Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile  
 210 215 220  
 Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser  
 225 230 235 240  
 Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr  
 245 250 255  
 Thr Trp Asp Lys Ile Lys  
 260

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG 60  
 TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA 120  
 ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA 180  
 TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA 240  
 TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACCC AAGAGTCTCC TTAAGGCAGG 300  
 CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT 360  
 ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT 420  
 G 421

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1      5      10      15
Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
20     25     30
Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
35     40     45
Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
50     55     60
Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65     70     75     80
Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
85     90     95
Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
100    105    110
Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
115    120    125
Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
130    135    140

```

## (2) INFORMATION FOR SEQ ID NO: 101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                331

```

## (2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp  
1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser  
20 25 30

Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala  
35 40 45

Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln  
50 55 60

Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu  
65 70 75 80

Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu  
85 90 95

Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

ATGGACAACA	GGAAACTGGG	ACGAGGTTAT	ATCTGGTAAG	ATTGACAAGT	ACAAAGATCC	60
AGATATTCCA	ACAGTTGAAT	CACAAGAAGT	TACGTCAGAC	TCTAGTGATA	AAGAAATAAC	120
GGTAAGGTAT	GACCGTTTAT	CAACACCAGA	AAAACCAATC	CCACAACCAA	ATCCAGAGCA	180
TCCAAGTGTT	CCGACACCAA	ACCCAGAACT	ACCAAATCAA	GAGACTCCAA	CACCAGATAA	240
ACCAACTCCA	GAACCAGGTA	CTCCAAAAAC	TGAAACTCCA	GTGAATCCAG	ACCCAGAAGT	300
TCCGACTTAT	GAGACAGGTA	AGAGAGAGGA	ATTGCCAAAC	ACAGGTACAG	AAGCTAAT	358

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Thr Thr Gly Asn Trp Asp Glu Val Ile Ser Gly Lys Ile Asp Lys  
 1 5 10 15  
 Tyr Lys Asp Pro Asp Ile Pro Thr Val Glu Ser Gln Glu Val Thr Ser  
 20 25 30  
 Asp Ser Ser Asp Lys Glu Ile Thr Val Arg Tyr Asp Arg Leu Ser Thr  
 35 40 45  
 Pro Glu Lys Pro Ile Pro Gln Pro Asn Pro Glu His Pro Ser Val Pro  
 50 55 60  
 Thr Pro Asn Pro Glu Leu Pro Asn Gln Glu Thr Pro Thr Pro Asp Lys  
 65 70 75 80  
 Pro Thr Pro Glu Pro Gly Thr Pro Lys Thr Glu Thr Pro Val Asn Pro  
 85 90 95  
 Asp Pro Glu Val Pro Thr Tyr Glu Thr Gly Lys Arg Glu Glu Leu Pro  
 100 105 110  
 Asn Thr Gly Thr Glu Ala Asn  
 115

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA 60  
 GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT 120  
 TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC 180  
 AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA 240  
 GCTAACAGAT GTCTTAAAG AACTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG 300  
 TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG 360  
 CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG 420  
 TGTAACCAA GTAATTCCTT ATGAATATT CGCTGGTGAT GGTATGTTAA CTCGTCTATT 480  
 ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT 540  
 ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA 600

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660  
 TTATAAAGCT ACTGTTAAAG TTTACGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720  
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780  
 AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840  
 AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900  
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960  
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020  
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAAACAAGC 1080  
 GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140  
 TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200  
 TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260  
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320  
 AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTTGACTCG 1380  
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTA AAAACCC 1440  
 AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500  
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560  
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620  
 CTTGGACAAC ATCGTAGCAA CTAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680  
 AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740  
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800  
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860  
 GTCAGAGGAT AAAGCTATG 1879

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser  
 1 5 10 15  
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu  
 20 25 30



Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro  
 35 40 45  
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser  
 50 55 60  
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu  
 65 70 75 80  
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly  
 85 90 95  
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly  
 100 105 110  
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu  
 115 120 125  
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val  
 130 135 140  
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu  
 145 150 155 160  
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys  
 165 170 175  
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe  
 180 185 190  
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala  
 195 200 205  
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr  
 210 215 220  
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu  
 225 230 235 240  
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys  
 245 250 255  
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp  
 260 265 270  
 Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr  
 275 280 285  
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly  
 290 295 300  
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser  
 305 310 315 320  
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn  
 325 330 335  
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn  
 340 345 350  
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa  
 355 360 365

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp  
 370 375 380  
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile  
 385 390 395 400  
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala  
 405 410 415  
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys  
 420 425 430  
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro  
 435 440 445  
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys  
 450 455 460  
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro  
 465 470 475 480  
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe  
 485 490 495  
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala  
 500 505 510  
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr  
 515 520 525  
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile  
 530 535 540  
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser  
 545 550 555 560  
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val  
 565 570 575  
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro  
 580 585 590  
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met  
 595 600 605  
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys  
 610 615 620  
 Ala Met  
 625

## (2) INFORMATION FOR SEQ ID NO: 107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60  
 TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120  
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180  
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240  
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300  
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360  
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420  
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480  
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540  
 CTTTGTGACT CAACACGCAg CCTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser Asn Gln Lys Gln Ala Asp Gly Lys Leu Asn Ile Val Thr Thr Phe  
 1 5 10 15  
 Tyr Pro Val Tyr Glu Phe Thr Lys Gln Val Ala Gly Asp Thr Ala Asn  
 20 25 30  
 Val Glu Leu Leu Ile Gly Ala Gly Thr Glu Pro His Glu Tyr Glu Pro  
 35 40 45  
 Ser Ala Lys Ala Val Ala Lys Ile Gln Asp Ala Asp Thr Phe Val Tyr  
 50 55 60  
 Glu Asn Glu Asn Met Glu Thr Trp Val Pro Lys Leu Leu Asp Thr Leu  
 65 70 75 80  
 Asp Lys Lys Lys Val Lys Thr Ile Lys Ala Thr Gly Asp Met Leu Leu  
 85 90 95  
 Leu Pro Gly Gly Glu Glu Glu Glu Gly Asp His Asp His Gly Glu Glu  
 100 105 110  
 Gly His His His Glu Phe Asp Pro His Val Trp Leu Ser Pro Val Arg  
 115 120 125  
 Ala Ile Lys Leu Val Glu His His Pro Arg His Leu Ser Ala Asp Tyr  
 130 135 140  
 Pro Asp Lys Lys Glu Thr Phe Glu Lys Asn Ala Ala Ala Tyr Ile Glu  
 145 150 155 160

Leu Asp Tyr Gly Thr  
195

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly  
 1 5 10 15  
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile  
 20 25 30  
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr  
 35 40 45  
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe  
 50 55 60  
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp  
 65 70 75 80  
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln  
 85 90 95  
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp  
 100 105 110  
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe  
 115 120 125  
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu  
 130 135 140  
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro  
 145 150 155 160  
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys  
 165 170 175  
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe  
 180 185 190  
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val  
 195 200 205  
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys  
 210 215 220  
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly  
 225 230 235 240  
 Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp Ile Thr Gly  
 245 250 255  
 Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg  
 260 265 270  
 Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala  
 275 280 285  
 Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val  
 290 295 300  
 Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu

305

310

315

320

Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu  
 325 330 335

## (2) INFORMATION FOR SEQ ID NO: 111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC 60  
 CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG 120  
 CGTCGCTATT TCTCTTGGA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGGAAATTGTC 180  
 CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTCAAA GGGGGGCTTT 240  
 GTCTCAGTAC CGCCTGTTAT CGCTGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA 300  
 TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTTGCGAC TAAGATGTAT 360  
 TCAACCTTTG AACAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG 412

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val  
 1 5 10 15  
 Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser  
 20 25 30  
 Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile  
 35 40 45  
 Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu  
 50 55 60  
 Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu  
 65 70 75 80  
 Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser  
 85 90 95  
 Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro

100

105

110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val  
 115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60  
 AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT 120  
 GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180  
 TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240  
 AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG 300  
 AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG 360  
 TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGTC TTACCGGCAG TTATCACTCC 420  
 GTTTGATACA ATAATGAAGG TGACTIONAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480  
 TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540  
 GAAT 544

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr  
 1 5 10 15

Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser  
 20 25 30

Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys  
 35 40 45

Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile

50	55	60
Val Pro Glu Ile Asp	Pro Ser Gln Ile Asp	Ser Arg Val Gln Ile Glu
65	70	75 80
Asn Val Met Val Ser	Asp Lys Glu Val Ser	Ile Thr Ser Asp Gln Glu
	85	90 95
Thr Leu Asp Arg Ile	Asp Lys Ile Ile Ala Val Leu Pro	Thr Ser Glu
	100	105 110
Arg Ile Thr Gly Asn Tyr	Ser Gly Ser Val Pro Leu Gln Ala Ile Asp	
	115	120 125
Arg Asn Gly Val Val Leu	Pro Ala Val Ile Thr Pro Phe Asp Thr Ile	
	130	135 140
Met Lys Val Thr Thr Lys	Pro Val Ala Pro Ser Ser Ser Thr Ser Asn	
	145	150 155 160
Ser Ser Thr Ser Ser Ser	Ser Ser Glu Thr Ser Ser Ser Thr Lys Ala Thr	
	165	170 175
Ser Ser Lys Thr Asn		
	180	

## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG	60
CGGTCTTGAG CAGGCAGGAA TTACCATTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA	120
TATGGAAATT ATCGCTGGAA ATGCCTTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC	180
GGACCAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA	240
CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAACT TCAACGACAG GTATGTTGTC	300
TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG	360
TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC	420
TTACCACCCA GAATACTCTA TTATCACCAA CATTGACTTT GACCATCCAG ATTATTTTAC	480
AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT	540
TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA	600
TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAGCTAGT GATCTTCTTC GTTCAATAAC	660
TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC	720
CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG	780



ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840  
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCACC ATCCAACAGA 900  
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960  
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020  
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080  
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140  
 TGTGAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200  
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260  
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr	1	5	10	15
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe	20	25	30	
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala	35	40	45	
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly	50	55	60	
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp	65	70	75	80
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr	85	90	95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu	100	105	110	
Ile	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Ser	Ala	Asn	Ala	Lys	Tyr	Phe	Val	115	120	125	
Phe	Glu	Ser	Asp	Glu	Tyr	Glu	Arg	His	Phe	Met	Pro	Tyr	His	Pro	Glu	130	135	140	
Tyr	Ser	Ile	Ile	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro	Asp	Tyr	Phe	Thr	145	150	155	160
Ser	Leu	Glu	Asp	Val	Phe	Asn	Ala	Phe	Asn	Asp	Tyr	Ala	Lys	Gln	Ile				

175

Leu Thr Ser Asn Val Gln  
420

GGTTTCTAAA	AGGGAAAATG	GAAAGAAACG	ACTTGTTTCAT	TTTCTGCTGT	TGACTAGCAT	120
GGGAGTTCAA	TTGTTGCCGG	CCAGTGCTTT	TGGGTTGACC	AGCCAGATTT	TATCTGCCTA	180
TAATAGTCAG	CTTTCTATCG	GAGTCGGGGA	ACATTTACCA	GAGCCTCTGA	AAATCGAAGG	240
TTATCAATAT	ATTGTTTATA	TCAAACTAA	GAAACAGGAT	AATACAGAGC	TTTCAAGGAC	300
AGTTGATGGG	AAATACTCTG	CTCAAAGAGA	TAGTCAACCA	AACTCTACAA	AAACATCAGA	360
TGTAGTTCAT	TCAGCTGATT	TAGAATGGAA	CCAAGGACAG	GGGAAGGTTA	GTTTACAAGG	420
TGAAGCATCA	GGGGATGATG	GACTTTTCAGA	AAAATCTTCT	ATAGCAGCAG	ACAATCTATC	480
TTCTAATGAT	TCATTGCGAA	GTCAAGTTGA	GCAGAATCCG	GATCACAAAAG	GAGAATCTGT	540
AGTTCGACCA	ACAGTGCCAG	AACAAGGAAA	TCCTGTGTCT	GCTACAACGG	TGCAGAGTGC	600
GGAAGAGGAA	GTATTGGCGA	CGACAAATGA	TCGACCAGAG	TATAAACTTC	CATTGGAAAC	660
CAAAGGCACG	CAAGAACCCG	GTCATGAGGG	TGAAGCCGCA	GTCCGTGAAG	ACTTACCAGT	720
CTACACTAAG	CCACTAGAAA	CCAAAGGTAC	ACAAGGACCC	GGACATGAAG	GTGAAGCTGC	780
AGTTCGCGAG	GAAGAACCAG	CTTACACAGA	ACCGTTAGCA	ACGAAAAGGCA	CGCAAGAGCC	840
AGGTCATGAG	GGCAAAGCTA	CAGTCCGCGA	AGAGACTCTA	GAGTACACGG	AACCGGTAGC	900
GACAAAAGGC	ACACAAGAAC	CCGAACATGA	GGGCGAaCGG	sCAGTAGAAG	AAGAACTTCC	960
GGCTTTTAGAG	GTCACTACAC	GAAATAGAAC	GGAAATCCAG	AATATTCCCTT	ATACAACAGA	1020
AGAAATTCAG	GATCCAACAC	TTCTGAAAAA	TCGTCGTAAG	ATTGAACGAC	AAGGGCAAGC	1080
AGGGACACGT	ACAATTCAAT	ATGAAGACTA	CATCGTAAAT	GGTAATGTCTG	TAGAAACTAA	1140
AGAAGTGTC	CGAACTGAAG	TAGCTCCGGT	CAACGAAGTC	GTTAAAGTAG	GAACACTTGT	1200
GAAAGTTAAA	CCTACAGTAG	AAATTACAAA	CTTAACAAAA	GTTGAGAACA	AAAAATCTAT	1260
AACTGTAAGT	TATAACTTAA	TAGACACTAC	CTCAGCATAT	GTTTCTGCAA	AAACGCAAGT	1320
TTTCCATGGA	GACAAGCTAG	TTAAAGAGGT	GGATATAGAA	AATCCTGCCA	AAGAGCAAGT	1380
AATATCAGGT	TTAGATTACT	ACACACCGTA	TACAGTTAAA	ACACACCTAA	CTTATAATTT	1440
GGGTGAAAAT	AATGAGGAAA	ATACTGAAAC	ATCAACTCAA	GATTTC CAAT	TAGAGTATAA	1500
GAAAATAGAG	ATTAAAGATA	TTGATTTCAGT	AGAATTATAC	GGTAAAGAAA	ATGATCGTTA	1560
TCGTAGATAT	TTAAGTCTAA	GTGAAGCGCC	GA CTGATACG	GCTAAATACT	TTGTAAAAGT	1620
GAAATCAGAT	CGCTTCAAAG	AAATGTACCT	ACCTGTAAAA	TCTATTACAG	AAAATACGGA	1680
TGGAACGTAT	AAAGTGACGG	TAGCCGTTGA	TCAACTTGTC	GAAGAAGGTA	CAGACGGTTA	1740
CAAAGATGAT	TACACATTTA	CTGTAGCTAA	ATCTAAAGCA	GAGCAACCAG	GAGTTTACAC	1800
ATCCTTTAAA	CAGCTGGTAA	CAGCCATGCA	AAGCAATCTG	TCTGGTGTCT	ATACATTGGC	1860
TTT CAGATATG	ACCGCAGATG	AGGTGAGCTT	AGGCGATAAG	CAGACAAGTT	ATCTCACAGG	1920

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 1980  
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 2040  
 TGTCTCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100  
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160  
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220  
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280  
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340  
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400  
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460  
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520  
 TGTTCATACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580  
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640  
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700  
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760  
 CAACATAGAA AAATGATGC CATTCTACAA TAAAGACCTA GTAGTTCATC ATGGTAACAA 2820  
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTGA GATGTTGTGC CGATGAAAGA 2880  
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940  
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 3000  
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060  
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120  
 C 3121

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30  
 His Phe Leu Leu Thr-Ser Met Gly Val Gln Leu Pro Ala Ser  
 35 40 45



Thr	Glu	Val	Ala	Pro	Val	Asn	Glu	Val	Val	Lys	Val	Gly	Thr	Leu	Val	385	390	395	400
Lys	Val	Lys	Pro	Thr	Val	Glu	Ile	Thr	Asn	Leu	Thr	Lys	Val	Glu	Asn	405	410		415
Lys	Lys	Ser	Ile	Thr	Val	Ser	Tyr	Asn	Leu	Ile	Asp	Thr	Thr	Ser	Ala	420	425		430
Tyr	Val	Ser	Ala	Lys	Thr	Gln	Val	Phe	His	Gly	Asp	Lys	Leu	Val	Lys	435	440		445
Glu	Val	Asp	Ile	Glu	Asn	Pro	Ala	Lys	Glu	Gln	Val	Ile	Ser	Gly	Leu	450	455		460
Asp	Tyr	Tyr	Thr	Pro	Tyr	Thr	Val	Lys	Thr	His	Leu	Thr	Tyr	Asn	Leu	465	470		480
Gly	Glu	Asn	Asn	Glu	Glu	Asn	Thr	Glu	Thr	Ser	Thr	Gln	Asp	Phe	Gln	485	490		495
Leu	Glu	Tyr	Lys	Lys	Ile	Glu	Ile	Lys	Asp	Ile	Asp	Ser	Val	Glu	Leu	500	505		510
Tyr	Gly	Lys	Glu	Asn	Asp	Arg	Tyr	Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	515	520		525
Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	530	535		540
Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	545	550		560
Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	565	570		575
Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	580	585		590
Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	595	600		605
Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	610	615		620
Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	625	630		640
Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	645	650		655
Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	660	665		670
Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	675	680		685
Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala	Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	690	695		700
Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly	Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	705	710		720

09765374 043300  
T00010 12059260

Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys  
 725 730 735  
 Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile  
 740 745 750  
 Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val  
 755 760 765  
 Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly  
 770 775 780  
 Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val  
 785 790 795 800  
 Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly  
 805 810 815  
 Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser  
 820 825 830  
 Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala  
 835 840 845  
 Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala  
 850 855 860  
 Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val  
 865 870 875 880  
 Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu  
 885 890 895  
 Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu  
 900 905 910  
 Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe  
 915 920 925  
 Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr  
 930 935 940  
 Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp  
 945 950 955 960  
 Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys  
 965 970 975  
 Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr  
 980 985 990  
 Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr  
 995 1000 1005  
 Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr  
 1010 1015 1020  
 Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn  
 1025 1030 1035 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA	ACTGTTGGTA	CTTTCCTTTT	TACTGCAGGA	TTGAGCTTGT	TAGTTTTATT	60
GGTTTCTAAA	AGGGAAAATG	GAAAGAAACG	ACTTGTTTCAT	TTTCTGCTGT	TGACTAGCAT	120
GGGAGTTCAA	TTGTTGCCCG	CCAGTGCTTT	TGGGTTGACC	AGCCAGATTT	TATCTGCCTA	180
TAATAGTCAG	CTTTCTATCG	GAGTCGGGGA	ACATTTACCA	GAGCCTCTGA	AAATCGAAGG	240
TTATCAATAT	ATTGGTTATA	TCAAACTAA	GAAACAGGAT	AATACAGAGC	TTTCAAGGAC	300
AGTTGATGGG	AAATACTCTG	CTCAAAGAGA	TAGTCAACCA	AACTCTACAA	AAACATCAGA	360
TGTAGTTCAT	TCAGCTGATT	TAGAATGGAA	CCAAGGACAG	GGGAAGGTTA	GTTTACAAGG	420
TGAAGCATCA	GGGGATGATG	GACTTTCAGA	AAAATCTTCT	ATAGCAGCAG	ACAATCTATC	480
TTCTAATGAT	TCATTGCGAA	GTCAAGTTGA	GCAGAATCCG	GATCACAAAAG	GAGAATCTGT	540
AGTTCGACCA	ACAGTGCCAG	AACAAGGAAA	TCCTGTGTCT	GCTACAACGG	TGCAGAGTGC	600
GGAAGAGGAA	GTATTGGCGA	CGACAAATGA	TCGACCAGAG	TATAAACTTC	CATTGGAAAC	660
CAAAGGCACG	CAAGAACCCG	GTCATGAGGG	TGAAGCCGCA	GTCCGTGAAG	ACTTACCAGT	720
CTACACTAAG	CCACTAGAAA	CCAAAGGTAC	ACAAGGACCC	GGACATGAAG	GTGAAGCTGC	780
AGTTCGCGAG	GAAGAACCAG	CTTACACAGA	ACCGTTAGCA	ACGAAAGGCA	CGCAAGAGCC	840
AGGTCATGAG	GGCAAAGCTA	CAGTCCGCGA	AGAGACTCTA	GAGTACACGG	AACCGGTAGC	900
GACAAAAGGC	ACACAAGAAC	CCGAACATGA	GGGCGAaCGG	sCAGTAGAAG	AAGAACTTCC	960
GGCTTTAGAG	GTCACTACAC	GAAATAGAAC	GGAAATCCAG	AATATTCCTT	ATACAACAGA	1020
AGAAATTCAG	GATCCAACAC	TTCTGAAAAA	TCGTCGTAAG	ATTGAACGAC	AAGGGCAAGC	1080
AGGGACACGT	ACAATTCAAT	ATGAAGACTA	CATCGTAAAT	GGTAATGTCG	TAGAAACTAA	1140
AGAAGTGTCa	CGAACTGAAG	TAGCTCCGGT	CAACGAAGTC	GTTAAAGTAG	GAACACTTGT	1200
GAAAGTTAAA	CCTACAGTAG	AAATTACAAA	CTTAACAAAA	GTTGAGAACA	AAAAATCTAT	1260
AACTGTAAGT	TATAACTTAA	TAGACACTAC	CTCAGCATAT	GTTTCTGCAA	AAACGCAAGT	1320
TTTCCATGGA	GACAAGCTAG	TTAAAGAGGT	GGATATAGAA	AATCCTGCCA	AAGAGCAAGT	1380
AATATCAGGT	TTAGATTACT	ACACACCGTA	TACAGTTAAA	ACACACCTAA	CTTATAATTT	1440
GGGTGAAAAT	AATGAGGAAA	ATACTGAAAC	ATCAACTCAA	GATTTCCAAT	TAGAGTATAA	1500
GAAAATAGAG	ATTAAAGATA	TTGATTCACT	AGAATTATAC	GGTAAAGAAA	ATGATCGTTA	1560
TCGTAGA						1567



## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30  
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser  
 35 40 45  
 Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu  
 50 55 60  
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly  
 65 70 75 80  
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu  
 85 90 95  
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln  
 100 105 110  
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu  
 115 120 125  
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly  
 130 135 140  
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser  
 145 150 155 160  
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys  
 165 170 175  
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val  
 180 185 190  
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr  
 195 200 205  
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln  
 210 215 220  
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val  
 225 230 235 240  
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu  
 245 250 255  
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu

236

260

265

270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg  
340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu  
355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg  
370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val  
385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn  
405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala  
420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys  
435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu  
450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu  
465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln  
485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu  
500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg  
515 520

## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT

60

102210: TCGTAGATAT

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 120  
 TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 180  
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 240  
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 300  
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 360  
 TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 420  
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 480  
 TGTCTTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 540  
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 600  
 AGCGAGCGCA ACAATAACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 660  
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 720  
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 780  
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 840  
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 900  
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 960  
 TGTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 1020  
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 1080  
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 1140  
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 1200  
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACCT ATGGTAACAA 1260  
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTGA GATGTTGTGC CGATGAAAGA 1320  
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 1380  
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 1440  
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 1500  
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 1560  
 C 1561

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	1	5	10	15
Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	20	25	30	
Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	35	40	45	
Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	50	55	60	
Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	65	70	75	80
Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	85	90	95	
Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	100	105	110	
Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	115	120	125	
Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	130	135	140	
Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	145	150	155	160
Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala	165	170	175	
Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly	180	185	190	
Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile	195	200	205	
Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys	Leu	Ile	Ala	Asn	His	Gln	Asp	Ser	210	215	220	
Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile	Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser	225	230	235	240
Ser	Arg	Val	Asn	Lys	Val	Arg	Val	Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala	245	250	255	
Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly	Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn	260	265	270	
Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val	Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly	275	280	285	
Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly	Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn	290	295	300	
Gly	Arg	Val	Asn	Asn	Val	Val	Ser	Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr	305	310	315	320

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Val Ile Thr Gly Asp Gln Tyr Ala Ala Asp Val Lys Asn Ala Ser  
 325 330 335

Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser  
 340 345 350

Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr  
 355 360 365

Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp  
 370 375 380

Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser  
 385 390 395 400

Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His  
 405 410 415

Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu  
 420 425 430

Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn  
 435 440 445

Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn  
 450 455 460

Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser  
 465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro  
 485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser  
 500 505 510

Asp Leu Gln Asn Val Thr Leu Asn  
 515 520

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG 60

TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA 120

GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA 180

AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA 240

AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA 300

ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA 360

CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420  
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480  
 TACTTCAATT GATGAAAGTA TGC GTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540  
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTA ACTACCG 600  
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660  
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720  
 TGATTGGGAT CTTGCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780  
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT 840  
 CAAAATCGT 850

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 283 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Phe Glu Gly Ser Lys Arg Gly Gln Phe Ala Val Glu Gly Ile  
 1 5 10 15  
 Asn Gln Leu Arg Glu His Val Asp Thr Leu Leu Ile Ile Ser Asn Asn  
 20 25 30  
 Asn Leu Leu Glu Ile Val Asp Lys Lys Thr Pro Leu Leu Glu Ala Leu  
 35 40 45  
 Ser Glu Ala Asp Asn Val Leu Arg Gln Gly Val Gln Gly Ile Thr Asp  
 50 55 60  
 Leu Ile Thr Asn Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Lys  
 65 70 75 80  
 Thr Val Met Ala Asn Lys Gly Asn Ala Leu Met Gly Ile Gly Ile Gly  
 85 90 95  
 Ser Gly Glu Glu Arg Val Val Glu Ala Ala Arg Lys Ala Ile Tyr Ser  
 100 105 110  
 Pro Leu Leu Glu Thr Thr Ile Asp Gly Ala Glu Asp Val Ile Val Asn  
 115 120 125  
 Val Thr Gly Gly Leu Asp Leu Thr Leu Ile Glu Ala Glu Glu Ala Ser  
 130 135 140  
 Gln Ile Val Asn Gln Ala Ala Gly Gln Gly Val Asn Ile Trp Leu Gly  
 145 150 155 160  
 Thr Ser Ile Asp Glu Ser Met Arg Asp Glu Ile Arg Val Thr Val Val  
 165 170 175

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Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln  
180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser  
195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro  
210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly  
225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val  
245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp  
260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg  
275 280

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTATTAG CTGATTTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG	540
AGCTTGGTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA	600
AGGACAATA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC	660
AGAAGGGGAG TGGGATTGA TTCCCTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA	720
CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTGGG CAGGTGCCTG ACTTAACTGG	900

TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCTCACA ACTGGTCCTA TCATTGGTTA 960  
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCTCTAA ATTACCCAAT 1020  
 TGAAAACTAT GTCAAACGAG TAAAAAGCGA A 1051

## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His  
 1 5 10 15  
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp  
 20 25 30  
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly  
 35 40 45  
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln  
 50 55 60  
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp  
 65 70 75 80  
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu  
 85 90 95  
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala  
 100 105 110  
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala  
 115 120 125  
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu  
 130 135 140  
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro  
 145 150 155 160  
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile  
 165 170 175  
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr  
 180 185 190  
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu  
 195 200 205  
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp  
 210 215 220  
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His

0076374 043304  
 T00010 725260



(2) INFORMATION FOR SEO ID NO: 127:

(A) LENGTH: 352 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TAAGGTCAA	AGTCAGACCG	CTAAGAAAGT	GCTAGAAAAG	ATTGGAGCTG	ACTCGGTTAT	60
CTCGCCAGAG	TATGAAATGG	GGCAGTCTCT	AGCACAGACC	ATTCTTTTCC	ATAATAGTGT	120
TGATGTCTTT	CAGTTGGATA	AAAATGTGTC	TATCGTGGAG	ATGAAAATTC	CTCAGTCTTG	180
GGCAGGTCAA	AGTCTGAGTA	AATTAGACCT	CCGTGGCAAA	TACAATCTGA	ATATTTTGGG	240
TTTCCGAGAG	CAGGAAAATT	CCCCATTGGA	TGTTGAATTT	GGACCAGATG	ACCTCTTGAA	300
AGCAGATACC	TATATTTTGG	CAGTCATCAA	CAACCAGTAT	TTGGATACCC	TA	352

(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala  
1 5 10 15

Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln  
20 25 30

Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn  
35 40 45

Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser  
50 55 60

Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly  
65 70 75 80

Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp  
85 90 95

Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln  
100 105 110

Tyr Leu Asp Thr Leu  
115

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA	60
TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT	120
GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG	180
TGCCTACTTG AAAATTCTTG AACTTGCAG GAAGTTGAGA GCAAAGGTCA AGAGGTGGAT	240
GTCTTTG	247

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser  
1 5 10 15

Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His  
20 25 30

Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

45

Ser Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1744 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TAGAGGCTTT	GCCAAATGGT	GGGAAGGGCA	CGAGCGTCGA	AAAGAGGAAC	GCTTTGTCAA	60
ACAAGAAGAA	AAAGCTCGCC	AAAAGGCTGA	GAAAGAGGCT	AGATTAGAAC	AAGAAGAGAC	120
TGAAAAAGCC	TTACTCGATT	TGCCTCCTGT	TGATATGGAA	ACGGGTGAAA	TTCTGACAGA	180
GGAAGCTGTT	CAAAATCTTC	CACCTATTCC	AGAAGAAAAG	TGGGTGGAAC	CAGAAAATCAT	240
CCTGCCTCAA	GCTGAACTTA	AATTCCCTGA	ACAGGAAGAT	GACTCAGATG	ACGAAGATGT	300
TCAGGTCGAT	TTTTCAGCCA	AAGAAGCCCT	TGAATACAAA	CTTCCAAGCT	TACAACTCTT	360
TGCACCAGAT	AAACCAAAG	ATCAGTCTAA	AGAGAAGAAA	ATTGTCAGAG	AAAATATCAA	420
AATCTTAGAA	GCAACCTTTG	CTAGCTTTGG	TATTAAGGTA	ACAGTTGAAC	GGGCCGAAAT	480
TGGGCCATCA	GTGACCAAGT	ATGAAGTCAA	GCCGGCTGTT	GGTGTAAGGG	TCAACCGCAT	540
TTCCAATCTA	TCAGATGACC	TCGCTCTAGC	CTTGGCTGCC	AAAGATGTCC	GGATTGAAGC	600
ACCAATCCCT	GGGAAATCCC	TAATCGGAAT	TGAAGTGCCC	AACTCCGATA	TTGCCACTGT	660
ATCTTTCCGA	GAACATATGGG	AACAATCGCA	AACGAAAGCA	GAAAATTTCT	TGGAAATTCC	720
TTTAGGGAAG	GCTGTTAATG	GAACCGCAAG	AGCTTTTGAC	CTTTCTAAAA	TGCCCCACTT	780
GCTAGTTGCA	GGTTCAACGG	GTTCAGGGAA	GTCAGTAGCA	GTTAACGGCA	TTATTGCTAG	840
CATTCTCATG	AAGGCGAGAC	CAGATCAAGT	TAAATTTATG	ATGGTCGATC	CCAAGATGGT	900
TGAGTTATCT	GTTTACAATG	ATATTCCCCA	CCTCTTGATT	CCAGTCGTGA	CCAATCCACG	960
CAAAGCCAGC	AAGGCTCTGC	AAAAGGTTGT	GGATGAAATG	GAAAACCGTT	ATGAACTCTT	1020
TGCCAAGGTG	GGAGTTCGGA	ATATTGCAGG	TTTTAATGCC	AAGGTAGAAG	AGTTCAATTC	1080
CCAGTCTGAG	TACAAGCAAA	TTCCGCTACC	ATTCATTGTC	GTGATTGTGG	ATGAGTTGGC	1140
TGACCTCATG	ATGGTGGCCA	GCAAGGAAGT	GGAAGATGCT	ATCATCCGTC	TTGGGCAGAA	1200

GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260  
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320  
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380  
 GCTCTTTTAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440  
 TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500  
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560  
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620  
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680  
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740  
 ACAA 1744

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu  
 1 5 10 15  
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu  
 20 25 30  
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro  
 35 40 45  
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln  
 50 55 60  
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile  
 65 70 75 80  
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp  
 85 90 95  
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr  
 100 105 110  
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln  
 115 120 125  
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala  
 130 135 140  
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile  
 145 150 155 160

Gly	Pro	Ser	Val	Thr	Lys	Tyr	Glu	Val	Lys	Pro	Ala	Val	Gly	Val	Arg
			165						170					175	
Val	Asn	Arg	Ile	Ser	Asn	Leu	Ser	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Ala
			180					185					190		
Ala	Lys	Asp	Val	Arg	Ile	Glu	Ala	Pro	Ile	Pro	Gly	Lys	Ser	Leu	Ile
		195					200					205			
Gly	Ile	Glu	Val	Pro	Asn	Ser	Asp	Ile	Ala	Thr	Val	Ser	Phe	Arg	Glu
	210					215					220				
Leu	Trp	Glu	Gln	Ser	Gln	Thr	Lys	Ala	Glu	Asn	Phe	Leu	Glu	Ile	Pro
225					230					235					240
Leu	Gly	Lys	Ala	Val	Asn	Gly	Thr	Ala	Arg	Ala	Phe	Asp	Leu	Ser	Lys
				245					250					255	
Met	Pro	His	Leu	Leu	Val	Ala	Gly	Ser	Thr	Gly	Ser	Gly	Lys	Ser	Val
			260					265					270		
Ala	Val	Asn	Gly	Ile	Ile	Ala	Ser	Ile	Leu	Met	Lys	Ala	Arg	Pro	Asp
		275					280					285			
Gln	Val	Lys	Phe	Met	Met	Val	Asp	Pro	Lys	Met	Val	Glu	Leu	Ser	Val
	290					295					300				
Tyr	Asn	Asp	Ile	Pro	His	Leu	Leu	Ile	Pro	Val	Val	Thr	Asn	Pro	Arg
305					310					315					320
Lys	Ala	Ser	Lys	Ala	Leu	Gln	Lys	Val	Val	Asp	Glu	Met	Glu	Asn	Arg
				325					330					335	
Tyr	Glu	Leu	Phe	Ala	Lys	Val	Gly	Val	Arg	Asn	Ile	Ala	Gly	Phe	Asn
			340					345					350		
Ala	Lys	Val	Glu	Glu	Phe	Asn	Ser	Gln	Ser	Glu	Tyr	Lys	Gln	Ile	Pro
		355					360					365			
Leu	Pro	Phe	Ile	Val	Val	Ile	Val	Asp	Glu	Leu	Ala	Asp	Leu	Met	Met
	370					375					380				
Val	Ala	Ser	Lys	Glu	Val	Glu	Asp	Ala	Ile	Ile	Arg	Leu	Gly	Gln	Lys
385					390					395					400
Ala	Arg	Ala	Ala	Gly	Ile	His	Met	Ile	Leu	Ala	Thr	Gln	Arg	Pro	Ser
				405					410					415	
Val	Asp	Val	Ile	Ser	Gly	Leu	Ile	Lys	Ala	Asn	Val	Pro	Ser	Arg	Val
			420					425					430		
Ala	Phe	Ala	Val	Ser	Ser	Gly	Thr	Asp	Ser	Arg	Thr	Ile	Leu	Asp	Glu
		435					440					445			
Asn	Gly	Ala	Glu	Lys	Leu	Leu	Gly	Arg	Gly	Asp	Met	Leu	Phe	Lys	Pro
	450					455					460				
Ile	Asp	Glu	Asn	His	Pro	Val	Arg	Leu	Gln	Gly	Ser	Phe	Ile	Ser	Asp
465					470					475					480
Asp	Asp	Val	Glu	Arg	Ile	Val	Asn	Phe	Ile	Lys	Thr	Gln	Ala	Asp	Ala
				485					490					495	

Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly  
 500 505 510  
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala  
 515 520 525  
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln  
 530 535 540  
 Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu  
 545 550 555 560  
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg  
 565 570 575  
 Lys Val Leu Gln Gln  
 580

## (2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 829 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGAAGTAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCTA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT	600
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA	829

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu  
 1 5 10 15  
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr  
 20 25 30  
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu  
 35 40 45  
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr  
 50 55 60  
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His  
 65 70 75 80  
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln  
 85 90 95  
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala  
 100 105 110  
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile  
 115 120 125  
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu  
 130 135 140  
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr  
 145 150 155 160  
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln  
 165 170 175  
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp  
 180 185 190  
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln  
 195 200 205  
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu  
 210 215 220  
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys  
 225 230 235 240  
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu  
 245 250 255  
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly  
 260 265 270  
 Leu Leu Lys Lys  
 275

(2) INFORMATION FOR SEQ ID NO: 135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA 60  
 AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT 120  
 CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG 180  
 AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGAATTGATG GATATCACAG ACGAAAAGGC 240  
 TGTTCCACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTAATATCGC 300  
 TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCGA 360  
 AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTTGAA AAACCAGCTC CAGAGGACGC 420  
 TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT 480  
 CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCCT 540  
 CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA 600  
 CAAGTTTGGC TTCATGAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA 660  
 TGATTTGAAG AATTACCTCA TCCAATTGG AAAAGAATTG ACTGAGAAGG AA 712

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn  
 1 5 10 15  
 Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr  
 20 25 30  
 Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu  
 35 40 45  
 Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe  
 50 55 60  
 Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala  
 65 70 75 80



251

Val	Pro	Leu	Thr	Lys	Gln	Leu	Met	Asp	Asp	Tyr	Glu	Arg	Thr	His	Ala	
				85					90					95		
Ser	Thr	Ile	Ala	Val	Met	Pro	Val	Pro	His	Asp	Glu	Val	Ser	Ala	Tyr	
			100					105					110			
Gly	Val	Ile	Ala	Pro	Gln	Gly	Glu	Gly	Lys	Asp	Gly	Leu	Tyr	Ser	Val	
		115					120					125				
Glu	Thr	Phe	Val	Glu	Lys	Pro	Ala	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	
		130				135					140					
Ala	Ile	Ile	Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu	Ile	Phe	Glu	Ile	Leu	
145					150					155					160	
Glu	Lys	Gln	Ala	Pro	Gly	Ala	Gly	Asn	Glu	Ile	Gln	Leu	Thr	Asp	Ala	
			165					170						175		
Ile	Asp	Thr	Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe	Ala	Arg	Glu	Phe	Lys	
			180					185					190			
Gly	Ala	Arg	Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly	Phe	Met	Lys	Thr	Ser	
		195					200					205				
Ile	Asp	Tyr	Ala	Leu	Lys	His	Pro	Gln	Val	Lys	Asp	Asp	Leu	Lys	Asn	
		210				215					220					
Tyr	Leu	Ile	Gln	Leu	Gly	Lys	Glu	Leu	Thr	Glu	Lys	Glu				
225					230					235						

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTTGAAAGC	60
CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC	120
TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AAAGTGGATT GTCCCTATGT	180
CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA	240
CTATCTCAAA ACAAACCTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC	300
AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCAGAGAC ATGCAGCGTG CTGGTCGCCT	360
GATTTTAAAA GAATTGGTC CTCAGTCTGT GGTTATCAAA GCGGACATC TCAAAGGTGG	420
TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA	480
AACCTGTCAC ACCCATGGTA CT	502

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala	Gln	Asn	Thr	Arg	Gly	Val	Gln	Leu	Ile	Glu	His	Val	Ser	Pro	Gln	1	5	10	15
Met	Leu	Lys	Ala	Gln	Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	20	25	30	
Ala	Val	Lys	Thr	Gly	Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	35	40	45	
Gln	Pro	Tyr	Leu	Lys	Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	50	55	60	
Met	Val	Ala	Thr	Ser	Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	65	70	75	80
Tyr	Leu	Lys	Thr	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	85	90	95	
Leu	Pro	Glu	Ala	Glu	Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	100	105	110	
Asp	Met	Gln	Arg	Ala	Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	115	120	125	
Ser	Val	Val	Ile	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe	130	135	140	
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln	145	150	155	160
Thr	Cys	His	Thr	His	Gly	Thr										165			

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA	TTAGAAAAG	ATAGCAAATC	AGACAAAGAA	CAAGTTGATA	AACTATTTGA	60
ATCATTTGAT	GCATCTTCAG	ATGAATCTAT	TTCTAAATTA	AAAGAACTAT	CTGAAACTTC	120
ACTTAAACC	GATGCAGGTA	AAGACTATCT	TAATAACAAA	GTCAAAGAAT	CATCTAAAGC	180
AATTGTAGAT	TTTCATTTC	AAAAGGTTT	GGCTTATGAT	GTAAAGATT	CAGATGACAA	240

ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT 300  
 TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTTG GAAGAAACTC TTAAATCTCT 360  
 AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA 420  
 AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG 480  
 TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC 540  
 TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA 600  
 TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC 660  
 AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720  
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGA ACTTTGGTGG 780  
 CGGCATTGCA GAACCTAGTC AACGC 805

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp  
 1 5 10 15  
 Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys  
 20 25 30  
 Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp  
 35 40 45  
 Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe  
 50 55 60  
 His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys  
 65 70 75 80  
 Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys  
 85 90 95  
 Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn  
 100 105 110  
 Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln  
 115 120 125  
 Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys  
 130 135 140  
 Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly  
 145 150 155 160

Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp  
 165 170 175

Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly  
 180 185 190

Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser  
 195 200 205

Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr  
 210 215 220

Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys  
 225 230 235 240

Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly  
 245 250 255

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg  
 260 265

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCTGACCAAG CAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT	60
GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAGTT	120
ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA	180
AAATGGAGGA GCAAATCGTA AAGTCAATGA T	211

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val	1 5 10 15
Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn	20 25 30
Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu	35 40 45

Asn Arg Lys Val Asn Asp  
65 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTCCGGCTCT	GTCCAGTCCA	CTTTTTCAGC	GGTAGAGGAA	CAGATTTTCT	TTATGGAGTT	60
TGAAGAACTC	TATCGGGAAA	CCCCAAAACG	CAGTGTAGCC	AGTCAGCAAA	AGACTAGTCT	120
GAACCTTAGAT	GGGCAGACGC	TTAGCAATGG	CAGTCAAAAG	TTGCCAGTCC	CTAAAGGAAT	180
TCAGGCCCCA	TCAGGCCAAA	GTATTACATT	TGACCGAGCT	GGGGGCAATT	CGTCCCTGGC	240
TAAGGTTGAA	TTTCAGACCA	GTAAAGGAGC	GATTCGCTAT	CAATTATATC	TAGGAAATGG	300
AAAAATTAAA	CGCATTAAGG	AAACAAAAAA	T			331

(i). SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser	Gly	Ser	Val	Gln	Ser	Thr	Phe	Ser	Ala	Val	Glu	Glu	Gln	Ile	Phe	
1				5					10					15		
Phe	Met	Glu	Phe	Glu	Glu	Leu	Tyr	Arg	Glu	Thr	Gln	Lys	Arg	Ser	Val	
			20					25					30			
Ala	Ser	Gln	Gln	Lys	Thr	Ser	Leu	Asn	Leu	Asp	Gly	Gln	Thr	Leu	Ser	
		35					40					45				
Asn	Gly	Ser	Gln	Lys	Leu	Pro	Val	Pro	Lys	Gly	Ile	Gln	Ala	Pro	Ser	
	50					55					60					
Gly	Gln	Ser	Ile	Thr	Phe	Asp	Arg	Ala	Gly	Gly	Asn	Ser	Ser	Leu	Ala	
65					70					75					80	
Lys	Val	Glu	Phe	Gln	Thr	Ser	Lys	Gly	Ala	Ile	Arg	Tyr	Gln	Leu	Tyr	
				85					90					95		
Leu	Gly	Asn	Gly	Lys	Ile	Lys	Arg	Ile	Lys	Glu	Thr	Lys	Asn			
			100					105					110			

## (2) INFORMATION FOR SEQ ID NO: 145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAAATC TTGCAAAAGG AAGAAGTCTT 60  
 GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA 120  
 GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT 180  
 GGCAATCAAA GAGCCA 196

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys  
 1 5 10 15  
 Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn  
 20 25 30  
 Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys  
 35 40 45  
 Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu  
 50 55 60  
 Pro  
 65

## (2) INFORMATION FOR SEQ ID NO: 147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT 60

095674 0460  
 12299260

(2) INFORMATION FOR SEQ ID NO:148:

(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg	Tyr	Gln	Gln	Gln	Ser	Glu	Gln	Lys	Glu	Trp	Leu	Leu	Phe	Val	Asp
1				5					10					15	
Gln	Leu	Glu	Val	Glu	Leu	Asp	Arg	Ser	Gln	Phe	Glu	Lys	Val	Glu	Gly
		20					25					30			
Asn	Arg	Leu	Tyr	Met	Lys	Gln	Asp	Gly	Lys	Asp	Ile	Ala	Ile	Gly	Lys
	35						40					45			
Ser	Lys	Ser	Asp	Asp	Phe	Arg	Lys	Thr	Asn	Ala	Arg	Gly	Arg	Gly	Tyr
	50					55					60				
Gln	Pro	Met	Val	Tyr	Gly	Leu	Lys	Ser	Val	Arg	Ile	Thr	Glu	Asp	Asn
65					70					75					80
Gln	Leu	Val	Arg	Phe	His	Phe	Gln	Phe	Gln	Lys	Gly	Leu	Glu	Arg	Glu
				85					90					95	
Phe	Ile	Tyr	Arg	Val	Glu	Lys	Glu	Lys	Ser						
			100					105							

(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GAACCGACAA	GTGCCCCACT	ATCAAGACTA	TGCTTTGAAT	AAAGAAAAAAT	TGGTTGCTTT	60
TGCTATGGCT	AAACGAACCA	AAGATAAGGT	TGAGCAAGAA	AGTGGGGAAC	AGTTTTTTTAA	120
TCTAGGTCAG	GTAAGCTATC	AAAACAAGAA	AACTGGCTTA	GTGACGAGGG	TTCGTACGGA	180
TAAGAGCCAA	TATGAGTTTC	TGTTTCCTTC	AGTCAAAATC	AAAGAAGAGA	AAAGAGATAA	240

(2) INFORMATION FOR SEQ ID NO:150:

(ii) MOLECULE TYPE: protein

Asn	Arg	Gln	Val	Ala	His	Tyr	Gln	Asp	Tyr	Ala	Leu	Asn	Lys	Glu	Lys
1			5					10						15	
Leu	Val	Ala	Phe	Ala	Met	Ala	Lys	Arg	Thr	Lys	Asp	Lys	Val	Glu	Gln
		20						25					30		
Glu	Ser	Gly	Glu	Gln	Phe	Phe	Asn	Leu	Gly	Gln	Val	Ser	Tyr	Gln	Asn
		35					40					45			
Lys	Lys	Thr	Gly	Leu	Val	Thr	Arg	Val	Arg	Thr	Asp	Lys	Ser	Gln	Tyr
	50					55					60				
Glu	Phe	Leu	Phe	Pro	Ser	Val	Lys	Ile	Lys	Glu	Glu	Lys	Arg	Asp	Lys
65					70					75					80
Lys	Glu	Glu	Val	Ala	Thr	Asp	Ser	Ser	Glu	Lys	Val	Glu	Lys	Lys	Lys
				85					90					95	
Ser	Glu	Glu	Lys	Pro	Glu	Lys	Lys	Glu	Asn	Ser					
			100					105							

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 784 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGTTGTCGGC	TGGCAATATA	TCCCGTTTCC	ATCTAAAGGT	AGTACAATTG	GTCTTACCC	60
AAATGGTATC	AGATTAGAAG	GTTTTCCAAA	GTCAGAGTGG	TACTACTTCG	ATAAAAATGG	120
AGTGCTACAA	GAGTTTGTTG	GTTGGAAAAC	ATTAGAGATT	AAAACATAAG	ACAGTGTTGG	180
AAGAAAGTAC	GGGGAAAAAC	GTGAAGATTC	AGAAGATAAA	GAAGAGAAGC	GTTATTATAC	240
GAACATTATC	TTTAATCAAA	ATCATTCTTT	AGAGACAGGT	TGGCTTTATG	ATCAGTCTAA	300
CTGGTATTAT	CTAGCTAAGA	CGGAAATTAA	TGGAGAAAAC	TACCTTGGTG	GTGAAAGACG	360



(2) INFORMATION FOR SEO ID NO:152:

(A) LENGTH: 261 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val	Val	Gly	Trp	Gln	Tyr	Ile	Pro	Phe	Pro	Ser	Lys	Gly	Ser	Thr	Ile
1				5					10					15	
Gly	Pro	Tyr	Pro	Asn	Gly	Ile	Arg	Leu	Glu	Gly	Phe	Pro	Lys	Ser	Glu
			20					25					30		
Trp	Tyr	Tyr	Phe	Asp	Lys	Asn	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Trp
		35					40					45			
Lys	Thr	Leu	Glu	Ile	Lys	Thr	Lys	Asp	Ser	Val	Gly	Arg	Lys	Tyr	Gly
	50					55					60				
Glu	Lys	Arg	Glu	Asp	Ser	Glu	Asp	Lys	Glu	Glu	Lys	Arg	Tyr	Tyr	Thr
65					70					75					80
Asn	Tyr	Tyr	Phe	Asn	Gln	Asn	His	Ser	Leu	Glu	Thr	Gly	Trp	Leu	Tyr
				85					90					95	
Asp	Gln	Ser	Asn	Trp	Tyr	Tyr	Leu	Ala	Lys	Thr	Glu	Ile	Asn	Gly	Glu
			100					105					110		
Asn	Tyr	Leu	Gly	Gly	Glu	Arg	Arg	Ala	Gly	Trp	Ile	Asn	Asp	Asp	Ser
		115					120					125			
Thr	Trp	Tyr	Tyr	Leu	Asp	Pro	Thr	Thr	Gly	Ile	Met	Gln	Thr	Gly	Trp
	130					135					140				
Gln	Tyr	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met
145					150					155					160
Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Gly	Thr	Thr	Trp	Tyr	Tyr	Leu	Asp	His
				165					170					175	
Pro	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Gln	Asn	Leu	Gly	Asn	Lys	Trp

260

180

185

190

Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp  
195 200 205

Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr  
210 215 220

Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly  
225 230 235 240

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn  
245 250 255

Gly Glu Trp Val Arg  
260

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAAGA AATGCTTGGG TAGGAAGTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGTTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTGG GGATAAGGAA TCTTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA	540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGTTT	600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT-TAETATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

00524 0430  
F0259260

TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080  
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140  
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200  
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260  
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320  
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTIONTTAA 1380  
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCCATTA GTGCCCTAGA 1440  
 AAGTAACTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500  
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560  
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA 1620  
 CAAGGCTTCT GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680  
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp  
 1 5 10 15

Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val  
 20 25 30

Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln  
 35 40 45

Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys  
 50 55 60

Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly  
 65 70 75 80

Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser  
 85 90 95

Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser  
 100 105 110

Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile  
 115 120 125

Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala  
 130 135 140



Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe Phe  
                                     485                                    490                                    495

Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr Phe  
                                     500                                    505                                    510

Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys Glu  
                                     515                                    520                                    525

Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser Gly  
                                     530                                    535                                    540

Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile Ala  
                                     545                                    550                                    555                                    560

Ser Val Met Met Lys Ile Asn Glu Lys  
                                     565

## (2) INFORMATION FOR SEQ ID NO: 155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATTTCAGAT GATTCTGAAG GATGGCAGTT TGTCCAAGAA AATGGTAGAA CCTACTACAA	60
AAAGGGGGAT CTAAAAGAAA CCTACTGGAG AGTGATAGAT GGGAAGTACT ATTATTTTGA	120
TCCTTTATCC GGAGAGATGG TTGTCGGCTG GCAATATATA CTGCTCCAC ACAAGGGGGT	180
TACGATTGGT CTTTCTCCAA GAATAGAGAT TGCTCTTAGA CCAGATTGGT TTTATTTTGG	240
TCAAGATGGT GTATTACAAG AATTTGTTGG CAAGCAAGTT TTAGAAGCAA AAAGTCTACT	300
GAATACCAAC AAACATCATG GGGAAGAATA TGATAGCCAA GCAGAGAAAC GAGTCTATTA	360
TTTTGAAGAT CAGCGTAGTT ATCATACTTT AAAAAGTGGT TGGATTTATG AAGAGGGTCA	420
TTGGTATTAT TTACAGAAGG ATGGTGGCTT TGATTCGCGC ATCAACAGAT TGACGGTTGG	480
AGAGCTAGCA CGTGGTTGGG TTAAGGATTA CCCTCTTACG TATGATGAAG AGAAGCTAAA	540
AGCAGCTCCA TGGTACTATC TAAATCCAGC AACTGGCATT ATGCAAACAG GTTGGCAATA	600
TCTAGGTAAT AGATGGTACT ACCTCCATTC GTCAGGAGCT ATGGCAACTG GCTGGTATAA	660
GGAAGGCTCA ACTTGGTACT ATCTAGATGC TGAAAATGGT GATATGAGAA CTGGCTGGCA	720
AAACCTTGGG AACAAATGGT ACTATCTCCG TTCATCAGGA GCTATGGCAA CTGGTTGGTA	780
TCAGGAAAGT TCGACTTGGT ACTATCTAAA TGCAAGTAAT GGAGATATGA AAACAGGCTG	840
GTTCCAAGTC AATGGTAACT GGTACTATGC CTATGATTCA GGTGCTTTAG CTGTTAATAC	900
CACAGTAGGT GGTACTACT TAACTATAA TGGTGAATGG GTTAAG	946

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly  
1 5 10 15

Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val  
20 25 30

Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val  
35 40 45

Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly  
50 55 60

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe  
65 70 75 80

Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu  
85 90 95

Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp  
100 105 110

Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr  
115 120 125

His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr  
130 135 140

Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val  
145 150 155 160

Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp  
165 170 175

Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr  
180 185 190

Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr  
195 200 205

Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser  
210 215 220

Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp  
225 230 235 240

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met  
245 250 255

Ala Thr Gly-Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala  
260 265 270

Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys  
305 310 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGTCGCTGCA	AATGAACTG	AAGTAGCAA	AAC TTCGAG	GATACAACGA	CAGCTTCAAG	60
TAGTTCAGAG	CAAAATCAGT	CTTCTAATAA	AACGCAAACG	AGCGCAGAAG	TACAGACTAA	120
TGCTGCTGCC	CACTGGGATG	GGGATTATTA	TGTAAAGGAT	GATGGTTCTA	AAGCTCAAAG	180
TGAATGGATT	TTTGACAACT	ACTATAAGGC	TTGGTTTTAT	ATTAATTCAG	ATGGTCGTTA	240
CTCGCAGAAT	GAATGGCATG	GAAATTACTA	CCTGAAATCA	GGTGGATATA	TGGCCCAAAA	300
CGAGTGGATC	TATGACAGTA	ATTACAAGAG	TTGGTTTTAT	CTCAAGTCAG	ATGGGGCTTA	360
TGCTCATCAA	GAATGGCAAT	TGATTGGAAA	TAAGTGGTAC	TACTTCAAGA	AGTGGGGTTA	420
CATGGCTAAA	AGCCAATGGC	AAGGAAGTTA	TTTCTTGAAT	GGTCAAGGAG	CTATGATGCA	480
AAATGAATGG	CTSCTATGAT	CCAGCCTATT	CTGCTTATTT	TTATCTAAAA	TCCGATGGAA	540
CTTATGCTAA	CCAAGAGTGG	CAAAAAGTGG	GCGGCAAATG	GTACTATTTT	AAGAAGTGGG	600
GCTATATGGC	TCGGAATGAG	TGGCAAGGCA	ACTACTATTT	GACTGGAAGT	GGTGCCATGG	660
CGACTGACGA	AGTGATTATG	GATGGTACTC	GCTATATCTT	TGCGGCCTCT	GGTGAGCTCA	720
AAGAAA AAAA	AGATTTGAAT	GTCGGCTGGG	TTCACAGAGA	TGGTAAGCGC	TATTTCTTTA	780
ATAATAGAGA	AGAACAAGTG	GGAACCGAAC	ATGCTAAGAA	AGTCATTGAT	ATTAGTGAGC	840
ACAATGGTCG	TATCAATGAT	TGGAAAAAGG	TTATTGATGA	GAACGAAGTG	GATGGTGTCA	900
TTGTTCTGCT	AGGTTATAGC	GGTAAAGAAG	ACAAGGAATT	GGCGCATAAC	ATTAAGGAGT	960
TAAACCGTCT	GGGAATTCCT	TATGGTGTCT	ATCTCTATAC	CTATGCTGAA	AATGAGACCG	1020
ATGCTGAGAG	TGACGCTAAA	CAGACCATTG	AAC TTATAAA	GAAATACAAT	ATGAACCTGT	1080
CTTACCC TAT	CTATTATGAT	GTTGAGAATT	GGGAATATGT	AAATAAGAGC	AAGAGAGCTC	1140
CAAGTGATAC	AGGCACTTGG	GTTAAAAATCA	TCAACAAGTA	CATGGACACG	ATGAAGCAGG	1200
CGGGTTTATCA	AAATGTGTAT	GTCTATAGCT	ATCGTAGTTT	ATTACAGACG	CGTTTAAAAAC	1260

ACCCAGATAT TTTAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320  
 AAAACCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380  
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr	1	5	10	15
Thr	Ala	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln		20	25	30	
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp	35	40	45	
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe	50	55	60	
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr	65	70	75	80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	85	90	95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe	100	105	110	
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile	115	120	125	
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser	130	135	140	
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln	145	150	155	160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys	165	170	175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys	180	185	190	
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln	195	200	205	
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val	210	215	220	
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys				



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225		230		235		240
Glu Lys Lys Asp	Leu Asn Val Gly Trp	Val His Arg Asp	Gly Lys Arg			
	245		250		255	
Tyr Phe Phe Asn	Asn Arg Glu Glu Gln	Val Gly Thr Glu	His Ala Lys			
	260		265		270	
Lys Val Ile Asp	Ile Ser Glu His Asn	Gly Arg Ile Asn	Asp Trp Lys			
	275		280		285	
Lys Val Ile Asp	Glu Asn Glu Val Asp	Gly Val Ile Val	Arg Leu Gly			
	290		295		300	
Tyr Ser Gly Lys	Glu Asp Lys Glu Leu	Ala His Asn Ile	Lys Glu Leu			
	305		310		315	
Asn Arg Leu Gly	Ile Pro Tyr Gly	Val Tyr Leu Tyr	Thr Tyr Ala Glu			
	325		330		335	
Asn Glu Thr Asp	Ala Glu Ser Asp	Ala Lys Gln Thr	Ile Glu Leu Ile			
	340		345		350	
Lys Lys Tyr Asn	Met Asn Leu Ser Tyr	Pro Ile Tyr Tyr	Asp Val Glu			
	355		360		365	
Asn Trp Glu Tyr	Val Asn Lys Ser Lys	Arg Ala Pro Ser	Asp Thr Gly			
	370		375		380	
Thr Trp Val Lys	Ile Ile Asn Lys Tyr	Met Asp Thr Met	Lys Gln Ala			
	385		390		395	
Gly Tyr Gln Asn	Val Tyr Val Tyr Ser	Tyr Arg Ser Leu	Leu Gln Thr			
	405		410		415	
Arg Leu Lys His	Pro Asp Ile Leu Lys	His Val Asn Trp	Val Ala Ala			
	420		425		430	
Tyr Thr Asn Ala	Leu Glu Trp Glu Asn	Pro His Tyr Ser	Gly Lys Lys			
	435		440		445	
Gly Trp Gln Tyr	Thr Ser Ser Glu Tyr	Met Lys Gly Ile	Gln Gly Arg			
	450		455		460	
Val Asp Val Ser	Val Trp Tyr					
	465		470			

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1924 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAATCTTC	60
ATTAGAGAAG AAATATGAGG AAGCAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA	120

AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC	180
TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT	240
TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC	300
TGACGCTGAA TATCAGAAAA AATTAACAGA GGTGCGACTCT AAAATAGAGA AGGCTAGGAA	360
AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC	420
AAATGCGTTG GCTGAGACTA AGAAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC	480
TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCACTA GCGAAGAAAG AAGTAGAGGC	540
TAAGGAACCT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC	600
TACTGCTCAA CATCAAGTAG ATAATTTGAA AAAACTTCTT GCTGGTGCGG ATCCTGATGA	660
TGGCACAGAA GTTATAGAAG CTAAATTAAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA	720
AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAAACTT CTTGACAGCC TTGATCCTGA	780
AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAAGC	840
TGATGAACTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATATT	900
ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA	960
AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCC	1020
TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC	1080
ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA	1140
ACCAGAGCAA CCAGCTCCAG CTCCAAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA	1200
GCAACCAGCT AAGCCGGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC	1260
TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC	1320
AATGGCAATA GGTTGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC	1380
TATGGCAACA GGTTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC	1440
TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG	1500
CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG	1560
TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTTCATGG TATTACCTCA ACGCTAATGG	1620
TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG	1680
TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG	1740
TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG	1800
TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT	1860
AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG	1920
GGTT	1924

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 641 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Thr	Ser	Gln	Pro	Thr	Phe	Val	Arg	Ala	Glu	Glu	Ser	Pro	Gln	Val	Val	1	5	10	15
Glu	Lys	Ser	Ser	Leu	Glu	Lys	Lys	Tyr	Glu	Glu	Ala	Lys	Ala	Lys	Ala	20	25	30	
Asp	Thr	Ala	Lys	Lys	Asp	Tyr	Glu	Thr	Ala	Lys	Lys	Lys	Ala	Glu	Asp	35	40	45	
Ala	Gln	Lys	Lys	Tyr	Glu	Asp	Asp	Gln	Lys	Arg	Thr	Glu	Glu	Lys	Ala	50	55	60	
Arg	Lys	Glu	Ala	Glu	Ala	Ser	Gln	Lys	Leu	Asn	Asp	Val	Ala	Leu	Val	65	70	75	80
Val	Gln	Asn	Ala	Tyr	Lys	Glu	Tyr	Arg	Glu	Val	Gln	Asn	Gln	Arg	Ser	85	90	95	
Lys	Tyr	Lys	Ser	Asp	Ala	Glu	Tyr	Gln	Lys	Lys	Leu	Thr	Glu	Val	Asp	100	105	110	
Ser	Lys	Ile	Glu	Lys	Ala	Arg	Lys	Glu	Gln	Gln	Asp	Leu	Gln	Asn	Lys	115	120	125	
Phe	Asn	Glu	Val	Arg	Ala	Val	Val	Val	Pro	Glu	Pro	Asn	Ala	Leu	Ala	130	135	140	
Glu	Thr	Lys	Lys	Lys	Ala	Glu	Glu	Ala	Lys	Ala	Glu	Glu	Lys	Val	Ala	145	150	155	160
Lys	Arg	Lys	Tyr	Asp	Tyr	Ala	Thr	Leu	Lys	Val	Ala	Leu	Ala	Lys	Lys	165	170	175	
Glu	Val	Glu	Ala	Lys	Glu	Leu	Glu	Ile	Glu	Lys	Leu	Gln	Tyr	Glu	Ile	180	185	190	
Ser	Thr	Leu	Glu	Gln	Glu	Val	Ala	Thr	Ala	Gln	His	Gln	Val	Asp	Asn	195	200	205	
Leu	Lys	Lys	Leu	Leu	Ala	Gly	Ala	Asp	Pro	Asp	Asp	Gly	Thr	Glu	Val	210	215	220	
Ile	Glu	Ala	Lys	Leu	Lys	Lys	Gly	Glu	Ala	Glu	Leu	Asn	Ala	Lys	Gln	225	230	235	240
Ala	Glu	Leu	Ala	Lys	Lys	Gln	Thr	Glu	Leu	Glu	Lys	Leu	Leu	Asp	Ser	245	250	255	
Leu	Asp	Pro	Glu	Gly	Lys	Thr	Gln	Asp	Glu	Leu	Asp	Lys	Glu	Ala	Glu	260	265	270	

T02210 12253260

Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala  
 275 280 285  
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala  
 290 295 300  
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys  
 305 310 315 320  
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn  
 325 330 335  
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro  
 340 345 350  
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro  
 355 360 365  
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro  
 370 375 380  
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu  
 385 390 395 400  
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu  
 405 410 415  
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp  
 420 425 430  
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn  
 435 440 445  
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly  
 450 455 460  
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala  
 465 470 475 480  
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val  
 485 490 495  
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser  
 500 505 510  
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln  
 515 520 525  
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr  
 530 535 540  
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly  
 545 550 555 560  
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu  
 565 570 575  
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr  
 580 585 590  
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe  
 595 600 605

Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala  
 610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp  
 625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA 60  
 ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA 120  
 TCCTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT 180  
 CTATGGTTAC TTGTCTATTC CAAGTTTGA AATCATGGAG CCGGTTTATT TGGGAGCAGA 240  
 TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG 300  
 TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTTCCG 360  
 CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420  
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480  
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCCTA CCTTTAATAA 540  
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC 600  
 TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660  
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu  
 1 5 10 15  
 Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 163:

(A) LENGTH: 784 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GATTGCTCCT	TTGAAGGATT	TGAGAGAAAC	CATGTTGGAA	ATTGCTTCTG	GTGCTCAAAA	60
TCTTCGTGCC	AAGGAAGTTG	GTGCCTATGA	ACTGAGAGAA	GTAAGTCGCC	AATTTAATGC	120
TATGTTGGAT	CAGATTGATC	AGTTGATGGT	AGCTATTCGT	AGCCAGGAAG	AAACGACCCG	180
TCAGTACCAA	CTTCAAGCCC	TTTCGAGCCA	GATTAATCCA	CATTTCCCTCT	ATAACACTTT	240
GGACACCATC	ATCTGGATGG	CTGAATTTCA	TGATAGTCAG	CGAGTGGTGC	AGGTGACCAA	300
GTCCTTGGCA	ACCTATTTCC	GCTTGGCGCT	CAATCAAGGC	AAGGACTTGA	TTTGTCTCTC	360
TGACGAAATC	AATCATGTCC	GCCAGTATCT	CTTTATCCAG	AAACAACGCT	ATGGAGATAA	420

GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480  
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540  
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600  
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660  
 TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720  
 GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780  
 TAGC 784

## (2) INFORMATION FOR SEQ ID NO:164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser  
 1 5 10 15  
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg  
 20 25 30  
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu  
 35 40 45  
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu  
 50 55 60  
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu  
 65 70 75 80  
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val  
 85 90 95  
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln  
 100 105 110  
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln  
 115 120 125  
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu  
 130 135 140  
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val  
 145 150 155 160  
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys  
 165 170 175  
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly  
 180 185 190

Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly  
 195 200 205  
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn  
 210 215 220  
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys  
 225 230 235 240  
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn  
 245 250 255  
 Arg Ile Glu Thr Ser  
 260

## (2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT 60  
 TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA 120  
 AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA 180  
 ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT 240  
 GGACAATGTC ATAAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA 300  
 AAAACGATTA AATGAGCTGA TAGAT 325

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile  
 1 5 10 15  
 Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His  
 20 25 30  
 Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys  
 35 40 45  
 Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly  
 50 55 60



Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met  
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala  
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp  
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA 60  
 TTTTGAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA 120  
 ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC 180  
 AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC 238

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln  
1 5 10 15

Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp  
20 25 30

His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe  
35 40 45

Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu  
50 55 60

Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CTACTATCAA TCAAGTTCTT CAGCCATTGA GGCCACCATT GAGGGCAACA GCCAAACGAC 60  
CATCAGCCAG ACTAGCCACT TTATTGAGTC TTATATCAAA AAAC TAGAAA CCACCTCGAC 120  
TGGTTTGACC CAGCAGACGG ATGTTCTGGC CTATGCTGAG AATCCCAGTC AAGACAAGGT 180  
CGAGGGAATC CGAGATTTGT TTTTGACCAT CTTGAAGTCA GATAAGGACT TGAAAACGTG 240  
TGTGCTGGTG ACCAAATCTG GTCAGGTCAT TTCTACAGAT GACAGTGTGC AGATGAAAAC 300  
TTCCTCTGAT ATGATGGCTG AGGATTGGTA CCAAAGGCC ATTCATCAGG GAGCTATGCC 360  
TGTTTTGACT CCAGCTCGTA AATCAGATAG TCAGTGGGTC ATTTCTGTCA CTCAAGAACT 420  
TGTTGATGCA AAGGGAGCCA ATCTTGGTGT GCTTCGTTTG GATATTTCTT ATGAAACTCT 480  
GGAAGCCTAT CTCAATCAAC TCCAGTTGGG GCAGCAGGGC TTTGCCTTCA TTATCAATGA 540  
AAACCATGAA TTTGTCTACC ATCCTCAACA CACAGTTTAT AGTTCGTCTA GCAAAATGGA 600  
GGCTATGAAA CCCTACATCG ATACAGGTCA GGGTTATACT CCTGGTCACA AATCCTACGT 660  
CAGTCAAGAG AAGATTGCAG GAACTGATTG GACGGTGCTT GCGGTGTCAT CATTGGAAAA 720  
GTTAGACCAG GTTCGGAGTC AG 742

## (2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 247 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr Tyr Gln Ser Ser Ser Ala Ile Glu Ala Thr Ile Glu Gly Asn  
1 5 10 15  
Ser Gln Thr Thr Ile Ser Gln Thr Ser His Phe Ile Gln Ser Tyr Ile  
20 25 30  
Lys Lys Leu Glu Thr Thr Ser Thr Gly Leu Thr Gln Gln Thr Asp Val  
35 40 45  
Leu Ala Tyr Ala Glu Asn Pro Ser Gln Asp Lys Val Glu Gly Ile Arg  
50 55 60  
Asp Leu Phe Leu Thr Ile Leu Lys Ser Asp Lys Asp Leu Lys Thr Val  
65 70 75 80  
Val Leu Val Thr Lys Ser Gly Gln Val Ile Ser Thr Asp Asp Ser Val  
85 90 95

Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys  
100 105 110

Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser  
115 120 125

Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys  
130 135 140

Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu  
145 150 155 160

Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe  
165 170 175

Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val  
180 185 190

Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr  
195 200 205

Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys  
210 215 220

Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys  
225 230 235 240

Leu Asp Gln Val Arg Ser Gln  
245

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA	60
GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAGGCCT ATGGTCTTCG	120
TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GGC GTGCAGT TTGCGGCCAA	180
GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG	240
TGCTGGTGAG TGGTCCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA	300
CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC	360
CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG	420
TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA	480
TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC	540
TCTTTCAAAC CACATGAGTA TGC GTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG	600

TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660  
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720  
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACTA 780  
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840  
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGAAGGTTG CCCAACGTGA 900  
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960  
 TCGTAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020  
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG 1080  
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA 1140  
 AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200  
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260  
 AACCAGCGTC ACAGTTCGTG CT 1282

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu  
 1 5 10 15  
 Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile  
 20 25 30  
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe  
 35 40 45  
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys  
 50 55 60  
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly  
 65 70 75 80  
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val  
 85 90 95  
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro  
 100 105 110  
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu  
 115 120 125  
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala  
 130 135 140

Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp  
 145 150 155 160  
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser  
 165 170 175  
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg  
 180 185 190  
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met  
 195 200 205  
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu  
 210 215 220  
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp  
 225 230 235 240  
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa  
 245 250 255  
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val  
 260 265 270  
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp  
 275 280 285  
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly  
 290 295 300  
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg  
 305 310 315 320  
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp  
 325 330 335  
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu  
 340 345 350  
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr  
 355 360 365  
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala  
 370 375 380  
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln  
 385 390 395 400  
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr  
 405 410 415  
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala  
 420 425

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60  
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120  
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180  
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240  
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300  
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360  
 CCTCTTGAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTAAACT 420  
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480  
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540  
 CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600  
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660  
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720  
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile  
 1 5 10 15  
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys  
 20 25 30  
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr  
 35 40 45  
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile  
 50 55 60  
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg  
 65 70 75 80  
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu  
 85 90 95  
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu  
 100 105 110

Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala  
 115 120 125  
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile  
 130 135 140  
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr  
 145 150 155 160  
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser  
 165 170 175  
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala  
 180 185 190  
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr  
 195 200 205  
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu  
 210 215 220  
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser  
 225 230 235 240  
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys  
 245 250 255  
 Met Ala Asn

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC 60  
 GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAACATCA 120  
 AATTATTATC ACTACACATT CTACACAACT TATAAAAGAT TTTCTAGAG AAGCCGTGAA 180  
 ACTTTTAGTG AAAACGGAG AAAAGGTAGA TGTTATTGAA AATATTGATT ATCAGGATGC 240  
 ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT 300  
 AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAGGT AGTGAGAATC TTAAACAGAA 360  
 TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAAA 420  
 CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA 480  
 TGTTAGTGAA TCAAATAATT TAATGAACTA TCTTGAAAT GGTGTTGTTA TATCAGATAA 540  
 AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC 600

660

694

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Ile Asp Tyr Trp Ala Lys Tyr  
225 230

(2) INFORMATION FOR SEQ ID NO: 177:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT 60  
 ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA 120  
 AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA 180  
 CACCATCAAT GATAATGCCT CTAGCATTCTG GCAAGGCATT CAAACTCTGA CAGGCAATCT 240  
 CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG 300  
 ACCTGCCTAT ATCGATTTTA TCGCCCCAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA 360  
 ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGTAAT AGGACTGGAA AGACTTATAG 420  
 TTATATTAC CCCATTTCCA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAAACTA 480  
 TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC 540  
 AACATCTGGC 550

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met  
 1 5 10 15  
 Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu  
 20 25 30  
 Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val  
 35 40 45  
 Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp  
 50 55 60  
 Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu  
 65 70 75 80  
 Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala  
 85 90 95  
 Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys

284

100	105	110
Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala		
115	120	125
Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro		
130	135	140
Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr		
145	150	155
Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe		
165	170	175
Thr Leu Phe Ser Thr Ser Gly		
180		

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA	60
GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTG CGCGACCCAG CAGAATTCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGGATTCT TGGAAAGGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val		
1	5	10
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp		
20	25	30
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg		
35	40	45

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys  
50 55 60

Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr  
65 70 75 80

Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile  
85 90 95

Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG	60
CAGCCAGTCA AGTCAGAAAA GTGAAACTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG	120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG	180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT	240
CTTGATGAAG GATCCAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG	300
TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC	360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA	420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA	480
TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC	540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC	600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC	660
AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA	720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA	780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG	840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT	900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAC TGGTCTACAG TTTCTACAAA	960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT	1020
AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT	1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC	1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC	1200

ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260  
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320  
 CAATCATTAT TTCTTCAAGA AG 1342

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser  
 1 5 10 15  
 Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro  
 20 25 30  
 Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile  
 35 40 45  
 Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His  
 50 55 60  
 Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu  
 65 70 75 80  
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn  
 85 90 95  
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val  
 100 105 110  
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu  
 115 120 125  
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn  
 130 135 140  
 Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp  
 145 150 155 160  
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala  
 165 170 175  
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp  
 180 185 190  
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys  
 195 200 205  
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn  
 210 215 220  
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

[illegible]

(2) INFORMATION FOR SEQ ID NO: 183:

(A) LENGTH: 934 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TGACTACCTT	GAAATCCCAC	TTTACAGCTA	TCTTGGTGGA	TTCAACACTA	AAGTTCCTCC	60
AACTCCAATG	ATGAACATCA	TCAACGGTGG	TTCTCACTCT	GACGCTCCAA	TCGCTTTCCA	120
AGAGTTCATG	ATCTTGCCAG	TTGGTGCGCC	AACATTAAAA	GAAGCCCTTC	GTTACGGTGC	180
TGAAATCTTC	CACGCTCTTA	AGAAAATCCT	TAAATCACGT	GGTTTGAAAA	CTGCCGTAGG	240
TGACGAAGGT	GGATTGCTC	CTCGTTTCGA	AGGAACTGAA	GATGGTGTTG	AAACTATCCT	300

TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360  
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420  
 TGAAGGTGCT GCTGTTTCGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480  
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGGAA 540  
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600  
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660  
 AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720  
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780  
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840  
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900  
 TCGTGGATTG AAATCATTCT ACAACCTTAA AAAA 934

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr  
 1 5 10 15  
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His  
 20 25 30  
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly  
 35 40 45  
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His  
 50 55 60  
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly  
 65 70 75 80  
 Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val  
 85 90 95  
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys  
 100 105 110  
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys  
 115 120 125  
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Ala Ala  
 130 135 140  
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn

10220: 4259250

145		150		155		160
Lys Tyr Pro Ile Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp						
	165			170		175
Asp Gly Trp Lys Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu						
	180			185		190
Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly						
	195			200		205
Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile						
	210			215		220
Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala						
	225			230		235
Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser						
	245			250		255
Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr						
	260			265		270
Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu						
	275			280		285
Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys						
	290			295		300
Ser Phe Tyr Asn Leu Lys Lys						
	305			310		

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTATCTTT TTTTGGAGCA ATGTTTCGCGT AGAAGGACAT TCCATGGATC CGACCCTAGC	60
GGATGGCGAA ATTCTCTTCG TTGTAAACA CCTTCCTATT GACCGTTTGT ATATCGTGGT	120
GGCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA	180
CACCATTCGT TACGAAAATG ATAAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA	240
TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAAACTC CAAAGCACTT ACTCAGGCAA	300
GGGCTTTGAA GGAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT	360
CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT	420
TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC	480
AAAAGATATC ACAGGGGAAG CTAAATTCCG CTTATGGCCA ATCACCCGTA TCGGAACATT	540

## (2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp  
 1 5 10 15  
 Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro  
 20 25 30  
 Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys  
 35 40 45  
 Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr  
 50 55 60  
 Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr  
 65 70 75 80  
 Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr  
 85 90 95  
 Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser  
 100 105 110  
 Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr  
 115 120 125  
 Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp  
 130 135 140  
 Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala  
 145 150 155 160  
 Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg  
 165 170 175  
 Ile Gly Thr Phe  
 180

## (2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA



GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC 120  
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180  
 GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240  
 TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAAGTC CTTGCCAAAG CCCAAAACCT 300  
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360  
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala  
 1 5 10 15

Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser  
 20 25 30

Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val  
 35 40 45

Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg  
 50 55 60

Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val  
 65 70 75 80

Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys  
 85 90 95

Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn  
 100 105 110

Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile  
 115 120 125

Leu Asp Lys Leu Lys  
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60  
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120  
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTA CT CAGGC TATTCTCAGT CAGCCATCTT 180  
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240  
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300  
 GACTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT 360  
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420  
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480  
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540  
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600  
 AACTCTTATC AATCTCCTTA TCGTTTTTTA TCCATTAGC TCGGGAGATA TCTTGCTGGA 660  
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720  
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780  
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840  
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900  
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960  
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020  
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCOA CCATTCAGGA 1080  
 TGCGGATTTA ATTCTTGCTT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140  
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200  
 A 1201

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile  
 1 5 10 15  
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln  
 20 25 30

Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His  
 35 40 45  
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr  
 50 55 60  
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu  
 65 70 75 80  
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val  
 85 90 95  
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro  
 100 105 110  
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala  
 115 120 125  
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu  
 130 135 140  
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile  
 145 150 155 160  
 Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile  
 165 170 175  
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val  
 180 185 190  
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg  
 195 200 205  
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile  
 210 215 220  
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu  
 225 230 235 240  
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe  
 245 250 255  
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Ala Lys Ala  
 260 265 270  
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr  
 275 280 285  
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu  
 290 295 300  
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu  
 305 310 315 320  
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln  
 325 330 335  
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala  
 340 345 350  
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val  
 355 360 365

Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg  
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG	60
AAAAGCAGTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC	120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC	180
CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAAC	240
AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT	300
CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAA AATAACAAG GAAATGATGT	360
GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTGG AAGTGATTAA	420
CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA	480
CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAA	540
TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA	600
TCCAAAACCA AGTGATGAGG AATTGAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC	660
CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG	720
TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAAGACA AATTGAGTC	780
TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA	840
AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT	900
TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG	960
CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT	1020
AGATTATGTT GAT	1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Arg	Asn	Ala	Gly	Gln	Thr	Asp	Ala	Ser	Gln	Ile	Glu	Lys	Ala	Ala	Val
1				5					10					15	
Ser	Gln	Gly	Gly	Lys	Ala	Val	Lys	Lys	Thr	Glu	Ile	Ser	Lys	Asp	Ala
			20					25					30		
Asp	Leu	His	Glu	Ile	Tyr	Leu	Ala	Gly	Gly	Cys	Phe	Trp	Gly	Val	Glu
		35					40					45			
Glu	Tyr	Phe	Ser	Arg	Val	Pro	Gly	Val	Thr	Asp	Ala	Val	Ser	Gly	Tyr
	50					55					60				
Ala	Asn	Gly	Arg	Gly	Glu	Thr	Thr	Lys	Tyr	Glu	Leu	Ile	Asn	Gln	Thr
65					70					75					80
Gly	His	Ala	Glu	Thr	Val	His	Val	Thr	Tyr	Asp	Ala	Lys	Gln	Ile	Ser
				85					90					95	
Leu	Lys	Glu	Ile	Leu	Leu	His	Tyr	Phe	Arg	Ile	Ile	Asn	Pro	Thr	Ser
			100					105					110		
Lys	Asn	Lys	Gln	Gly	Asn	Asp	Val	Gly	Thr	Gln	Tyr	Arg	Thr	Gly	Val
		115					120					125			
Tyr	Tyr	Thr	Asp	Asp	Lys	Asp	Leu	Glu	Val	Ile	Asn	Gln	Val	Phe	Asp
	130					135					140				
Glu	Val	Ala	Lys	Lys	Tyr	Asp	Gln	Pro	Leu	Ala	Val	Glu	Lys	Glu	Asn
145					150					155					160
Leu	Lys	Asn	Phe	Val	Val	Ala	Glu	Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys
				165					170					175	
Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His	Ile	Asn	Val	Asn	Gln	Ala	Ala	Tyr
			180					185					190		
Pro	Val	Ile	Asp	Ala	Ser	Lys	Tyr	Pro	Lys	Pro	Ser	Asp	Glu	Glu	Leu
		195					200					205			
Lys	Lys	Thr	Leu	Ser	Pro	Glu	Glu	Tyr	Ala	Val	Thr	Gln	Glu	Asn	Gln
	210					215					220				
Thr	Glu	Arg	Ala	Phe	Ser	Asn	Arg	Tyr	Trp	Asp	Lys	Phe	Glu	Ser	Gly
225					230					235					240
Ile	Tyr	Val	Asp	Ile	Ala	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp
			245						250					255	
Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Thr	Gln	Pro	Ile	Ser
			260					265					270		
Pro	Asp	Val	Val	Thr	Tyr	Lys	Glu	Asp	Lys	Ser	Tyr	Asn	Met	Thr	Arg
		275					280					285			
Met	Glu	Val	Arg	Ser	Arg	Val	Gly	Asp	Ser	His	Leu	Gly	His	Val	Phe
290						295					300				
Thr	Asp	Gly	Pro	Gln	Asp	Lys	Gly	Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser
305					310					315					320

Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr  
 325 330 335

Ala Tyr Leu Leu Asp Tyr Val Asp  
 340

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA	60
GAGCATGCGC CTGATAAAAT AGTTTTAGAT CATGCTTTTCG GTCAAACATAT ATTAGATAAA	120
AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA	180
ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTA GTGCTGATAA AGGAGTTTAA	240
CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG	300
GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT	360
TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA	396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu	1 5 10 15
Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala	20 25 30
Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile	35 40 45
Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val	50 55 60
Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu	65 70 75 80
Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu	85 90 95

F00271.0226

Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys  
 100 105 110

Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr  
 115 120 125

Asp Thr Leu Ser  
 130

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAAATATA GAAATTATTT TAGTTGATGA	60
CGGTTCTACG GATAATTCTG GGGAAATTG TGATGCTTTT ATGATGCAAG ATAATCGTGT	120
GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG	180
TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTCAGAT GATATCGTAA AAGAAAATAT	240
GATTGAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA	300
CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTTTAT GTAACAGGGC AAGATTTTTG	360
CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA	420
TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT	480
TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT	540
AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG	600
CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTTTTCTAA	660
GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT	720
CAATCTTTTA AAAGATTATA AGCAAACCTT AGAATACCAT CAATTAACAG ATACTGAGGA	780
ATATAAAGAT ATTTGTTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA	840
AAGT	844

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

F026274.04204

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys	Val	Glu	His	Ile	Leu	Lys	Gln	Thr	Tyr	Gln	Asn	Ile	Glu	Ile	Ile		
1				5					10					15			
Leu	Val	Asp	Asp	Gly	Ser	Thr	Asp	Asn	Ser	Gly	Glu	Ile	Cys	Asp	Ala		
		20						25					30				
Phe	Met	Met	Gln	Asp	Asn	Arg	Val	Arg	Val	Leu	His	Gln	Glu	Asn	Lys		
		35					40					45					
Gly	Gly	Ala	Ala	Gln	Ala	Lys	Asn	Met	Gly	Ile	Ser	Val	Ala	Lys	Gly		
	50					55					60						
Glu	Tyr	Ile	Thr	Ile	Val	Asp	Ser	Asp	Asp	Ile	Val	Lys	Glu	Asn	Met		
65					70					75					80		
Ile	Glu	Thr	Leu	Tyr	Gln	Gln	Val	Gln	Glu	Lys	Asp	Ala	Asp	Val	Val		
				85					90					95			
Ile	Gly	Asn	Tyr	Tyr	Asn	Tyr	Asp	Glu	Ser	Asp	Gly	Asn	Phe	Tyr	Phe		
		100						105					110				
Tyr	Val	Thr	Gly	Gln	Asp	Phe	Cys	Val	Glu	Glu	Leu	Ala	Ile	Gln	Glu		
		115					120					125					
Ile	Met	Asn	Arg	Gln	Ala	Gly	Asp	Trp	Lys	Phe	Asn	Ser	Ser	Ala	Phe		
	130					135					140						
Ile	Leu	Pro	Thr	Phe	Lys	Leu	Ile	Lys	Lys	Glu	Leu	Phe	Asn	Glu	Val		
145					150					155					160		
His	Phe	Ser	Asn	Gly	Arg	Arg	Phe	Asp	Asp	Glu	Ala	Thr	Met	His	Arg		
				165					170					175			
Phe	Tyr	Leu	Leu	Ala	Ser	Lys	Ile	Val	Phe	Ile	Asn	Asp	Asn	Leu	Tyr		
		180						185					190				
Leu	Tyr	Arg	Arg	Arg	Ser	Gly	Ser	Ile	Met	Arg	Thr	Glu	Phe	Asp	Leu		
	195						200					205					
Ser	Trp	Ala	Arg	Asp	Ile	Val	Glu	Val	Phe	Ser	Lys	Lys	Ile	Ser	Asp		
	210					215					220						
Cys	Val	Leu	Ala	Gly	Leu	Asp	Val	Ser	Val	Leu	Arg	Ile	Arg	Phe	Val		
225					230					235					240		
Asn	Leu	Leu	Lys	Asp	Tyr	Lys	Gln	Thr	Leu	Glu	Tyr	His	Gln	Leu	Thr		
			245						250					255			
Asp	Thr	Glu	Glu	Tyr	Lys	Asp	Ile	Cys	Phe	Arg	Leu	Lys	Leu	Phe	Phe		
		260						265					270				
Asp	Ala	Glu	Gln	Arg	Asn	Gly	Lys	Ser									
	275						280										

## (2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

F00001-01200



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTGAGA ATCAGACGTA TCAAAATTTT GAGTGTATAT TAATCAATGA 60  
 TGGCTCTCCA GATCATTGAT CCAAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120  
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180  
 TTCGGGGGGG GCGTACATTA CTTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240  
 AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GCGTTATAA 300  
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360  
 AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420  
 GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480  
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540  
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600  
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660  
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720  
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTACAG 780  
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu  
 1 5 10 15  
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu  
 20 25 30  
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly  
 35 40 45  
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala  
 50 55 60  
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu  
 65 70 75 80  
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile  
 85 90 95

300.

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr  
100 105 110

Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile  
115 120 125

Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val  
130 135 140

Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe  
145 150 155 160

Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu  
165 170 175

Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr  
180 185 190

Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg  
195 200 205

Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala  
210 215 220

Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg  
225 230 235 240

Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr  
245 250 255

Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro  
260 265 270

(2). INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA	60
TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT	120
TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA	180
TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT	240
AGAAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA	300
TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA	360
GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGTAT GAAACTCAAG AAATGAAGAG	420
TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG	480
CTTTGACATA GGTAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC	540

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600  
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660  
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720  
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780  
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840  
 GAAAGCCATT GTCCTCGCAG CAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA 900  
 GTCTATTTGT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960  
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020  
 TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080  
 ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140  
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200  
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260  
 TCTCTTGGTA AACAATGCTT TTTGGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320  
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380  
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440  
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCATC ATCTTTCTCA 1500  
 TCGGAAACCG TGGAAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560  
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620  
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680  
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTTAAGATAG CAGCTAGAGT 1740  
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800  
 AATTCATCTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860  
 TATTAATCAT GCGGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920  
 TATCTTATCC TTTGAAAATA CTAAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980  
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

\_\_\_\_(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Cys 1	Leu	Asp	Ser	Ile 5	Ile	Thr	Gln	Thr	Tyr 10	Lys	Asn	Ile	Glu	Ile 15	Val
Val	Val	Asn	Asp 20	Gly	Ser	Thr	Asp	Ala 25	Ser	Gly	Glu	Ile	Cys 30	Lys	Glu
Phe	Ser	Glu 35	Met	Asp	His	Arg	Ile 40	Leu	Tyr	Ile	Glu	Gln 45	Glu	Asn	Ala
Gly	Leu 50	Ser	Ala	Ala	Arg	Asn 55	Thr	Gly	Leu	Asn	Asn 60	Met	Ser	Gly	Asn
Tyr 65	Val	Thr	Phe	Val 70	Asp	Ser	Asp	Asp	Trp	Ile 75	Glu	Gln	Asp	Tyr 80	Val
Glu	Thr	Leu	Tyr	Lys 85	Lys	Ile	Val	Glu	Tyr 90	Gln	Ala	Asp	Ile	Ala 95	Val
Gly	Asn	Tyr	Tyr 100	Ser	Phe	Asn	Glu	Ser 105	Glu	Gly	Met	Phe	Tyr 110	Phe	His
Ile	Leu	Gly 115	Asp	Ser	Tyr	Tyr	Glu 120	Lys	Val	Tyr	Asp	Asn 125	Val	Ser	Ile
Phe	Glu 130	Asn	Leu	Tyr	Glu	Thr 135	Gln	Glu	Met	Lys	Ser	Phe	Ala	Leu	Ile
Ser 145	Ala	Trp	Gly	Lys 150	Leu	Tyr	Lys	Ala	Arg	Leu 155	Phe	Glu	Gln	Leu	Arg 160
Phe	Asp	Ile	Gly	Lys 165	Leu	Gly	Glu	Asp	Gly 170	Tyr	Leu	Asn	Gln	Lys 175	Val
Tyr	Leu	Leu 180	Ser	Glu	Lys	Val	Ile 185	Tyr	Leu	Asn	Lys	Ser	Leu 190	Tyr	Ala
Tyr	Arg 195	Ile	Arg	Lys	Gly	Ser	Leu 200	Ser	Arg	Val	Trp	Thr 205	Glu	Lys	Trp
Met 210	His	Ala	Leu	Val	Asp	Ala 215	Met	Ser	Glu	Arg	Ile 220	Thr	Leu	Leu	Ala
Asn 225	Met	Gly	Tyr	Pro	Leu 230	Glu	Lys	His	Leu	Ala 235	Val	Tyr	Arg	Gln	Met 240
Leu	Glu	Val	Ser	Leu 245	Ala	Asn	Gly	Gln	Ala 250	Ser	Gly	Leu	Ser	Asp 255	Thr
Ala	Thr	Tyr	Lys 260	Glu	Phe	Glu	Met	Lys 265	Gln	Arg	Leu	Leu	Asn 270	Gln	Leu
Ser	Arg	Gln 275	Glu	Glu	Ser	Glu	Lys 280	Lys	Ala	Ile	Val	Leu 285	Ala	Ala	Asn
Tyr 290	Gly	Tyr	Val	Asp	Gln 295	Val	Leu	Thr	Thr	Ile	Lys 300	Ser	Ile	Cys	Tyr
His 305	Asn	Arg	Ser	Ile 310	Arg	Phe	Tyr	Leu	Ile	His 315	Ser	Asp	Phe	Pro	Asn 320
Glu	Trp	Ile	Lys 325	Gln	Leu	Asn	Lys	Arg	Leu 330	Glu	Lys	Phe	Asp	Ser	Glu 335

Ile	Ile	Asn	Cys	Arg	Val	Thr	Ser	Glu	Ile	Ser	Cys	Tyr	Lys	Ser	
			340					345				350			
Asp	Ile	Ser	Tyr	Thr	Val	Phe	Leu	Arg	Tyr	Phe	Ile	Ala	Asp	Phe	Val
		355					360					365			
Gln	Glu	Asp	Lys	Ala	Leu	Tyr	Leu	Asp	Cys	Asp	Leu	Val	Val	Thr	Lys
	370					375					380				
Asn	Leu	Asp	Asp	Leu	Phe	Ala	Thr	Asp	Leu	Gln	Asp	Tyr	Pro	Leu	Ala
385					390					395					400
Ala	Val	Arg	Asp	Phe	Gly	Gly	Arg	Ala	Tyr	Phe	Gly	Gln	Glu	Ile	Phe
				405					410					415	
Asn	Ala	Gly	Val	Leu	Leu	Val	Asn	Asn	Ala	Phe	Trp	Lys	Lys	Glu	Asn
			420					425					430		
Met	Thr	Gln	Lys	Leu	Ile	Asp	Val	Thr	Asn	Glu	Trp	His	Asp	Lys	Val
		435					440					445			
Asp	Gln	Ala	Asp	Gln	Ser	Ile	Leu	Asn	Met	Leu	Phe	Glu	His	Lys	Trp
	450					455					460				
Leu	Glu	Leu	Asp	Phe	Asp	Tyr	Asn	His	Ile	Val	Ile	His	Lys	Gln	Phe
465					470					475					480
Ala	Asp	Tyr	Gln	Leu	Pro	Glu	Gly	Gln	Asp	Tyr	Pro	Ala	Ile	Ile	His
				485					490					495	
Tyr	Leu	Ser	His	Arg	Lys	Pro	Trp	Lys	Asp	Leu	Ala	Ala	Gln	Thr	Tyr
			500					505					510		
Arg	Glu	Val	Trp	Trp	Tyr	Tyr	His	Gly	Leu	Glu	Trp	Thr	Glu	Leu	Gly
		515					520					525			
Gln	Asn	His	His	Leu	His	Pro	Leu	Gln	Arg	Ser	His	Ile	Tyr	Pro	Ile
	530					535					540				
Lys	Glu	Pro	Phe	Thr	Cys	Leu	Ile	Tyr	Thr	Ala	Ser	Asp	His	Ile	Glu
545					550					555					560
Gln	Ile	Glu	Thr	Leu	Val	Gln	Ser	Leu	Pro	Asp	Ile	Gln	Phe	Lys	Ile
				565					570					575	
Ala	Ala	Arg	Val	Ile	Val	Ser	Asp	Arg	Leu	Ala	Gln	Met	Thr	Ile	Tyr
			580					585					590		
Pro	Asn	Val	Thr	Ile	Phe	Asn	Gly	Ile	His	Tyr	Leu	Val	Asp	Val	Asp
		595					600					605			
Asn	Glu	Leu	Val	Glu	Thr	Ser	Gln	Val	Leu	Leu	Asp	Ile	Asn	His	Gly
	610					615					620				
Glu	Lys	Thr	Glu	Glu	Ile	Leu	Asp	Gln	Phe	Ala	Asn	Leu	Gly	Lys	Pro
625					630					635					640
Ile	Leu	Ser	Phe	Glu	Asn	Thr	Lys	Thr	Tyr	Glu	Val	Gly	Gln	Glu	Ala
				645					650					655	
Tyr	Ala	Val	Asp	Gln	Val	Gln	Ala	Met	Ile	Glu	Lys	Leu	Arg	Glu	Ile
			660					665					670		

Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA	60
TGAAAGTGGT CGCTTGTTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA	120
TAAAAAGAAC GAAGGATTGT CGCAAGCAGC AAATGATGGG ATGAAGCAGG CTCACGGGGA	180
TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA	240
TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC	300
TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC	360
ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT	420
CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA	480
TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCATTATTA	540
TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC	600
CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA	660
AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT	720
AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAAGGCCA	780
TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC	840
CCTATTCATA AATATTCCT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA	900
AAAATTACAT	910

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile	Gln	Lys	Gln	Thr	Tyr	Gln	Asn	Leu	Glu	Ile	Ile	Leu	Val	Asp	Asp
1				5					10					15	

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln  
 20 25 30  
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln  
 35 40 45  
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe  
 50 55 60  
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr  
 65 70 75 80  
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met  
 85 90 95  
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp  
 100 105 110  
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly  
 115 120 125  
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile  
 130 135 140  
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr  
 145 150 155 160  
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr  
 165 170 175  
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys  
 180 185 190  
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe  
 195 200 205  
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe  
 210 215 220  
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu  
 225 230 235 240  
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe  
 245 250 255  
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys  
 260 265 270  
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr  
 275 280 285  
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His  
 290 295 300

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TAAGGCTGAT	AATCGTGTTT	AAATGAGAAC	GACGATTAAT	AATGAATCGC	CATTGTTGCT	60
TTCTCCGTTG	TATGGCAATG	ATAATGGTAA	CGGATTATGG	TGGGGGAACA	CATTGAAGGG	120
AGCATGGGAA	GCTATTCTCTG	AAGATGTAAA	GCCATATGCA	GCGATTGAAC	TTCATCTCTG	180
AAAAGTCTGT	AAACCAACAA	GTTGTATTCC	ACGAGATACG	AAAGAATTGA	GAGAATGGTA	240
TGTCAAGATG	TTGGAGGAAG	CTCAAAGTCT	AAACATTCCA	GTTTCTTGG	TTATTATGTC	300
GGCTGGAGAG	CGTAATACAG	TTCTCCAGA	GTGGTTAGAT	GAACAATTCC	AAAAGTATAG	360
TGTGTTAAAA	GGTGTTTTAA	ATATTGAGAA	TTATTGGATT	TACAATAACC	AGTTAGCTCC	420
GCATAGTGCT	AAATATTTGG	AAGTTTGTGC	CAAATATGGA	GCGCATTTTA	TCTGGCATGA	480
TCATGAAAAA	TGGTTCTGGG	AACTATTAT	GAATGATCCG	ACATTCTTTG	AAGCGAGTCA	540
AAAATATCAT	AAAAATTTGG	TGTTGGCAAC	TAAAAATACG	CCAATAAGAG	ATGATGCGGG	600
TACAGATTCT	ATCGTTAGTG	GATTTTGGTT	GAGTGGCTTA	TGTGATAACT	GGGGCTCATC	660
AACAGATACA	TGGAAATGGT	GGGAAAAACA	TTATACAAAC	ACATTTGAAA	CTGGAAGAGC	720
TAGGGATATG	AGATCCTATG	CATCGGAACC	AGAATCAATG	ATTGCTATGG	AAATGATGAA	780
TGTATATACT	GGGGGAGGCA	CAGTTTATAA	TTTCGAATGT	GCCGCGTATA	CATTTATGAC	840
AAATGATGTA	CCAATCCAG	CATTTACTAA	AGGTATTATT	CCTTCTTTA	GACATGCTAT	900
ACAAAATCCA	GCTCCAAGTA	AGGAAGAAGT	TGTAAATAGA	ACAAAAGCTG	TATTTTGGAA	960
TGGAGAAGGT	AGGATTAGTT	CATTAAACGG	ATTTTATCAA	GGAATTTATT	CGAATGATGA	1020
AACAATGCCT	TTATATAATA	ATGGGAGATA	TCATATTCTT	CCTGTAATAC	ATGAGAAAAT	1080
TGATAAGGAA	AAGATTTTAT	CTATATTCCC	TAATGCAAAA	ATTTTGACTA	AAAATAGTGA	1140
GGAATTGTCT	AGTAAAGTCA	ACTATTTAAA	CTCGCTTTAT	CCAAAACCTT	ATGAAGGAGA	1200
TGGGTATGCT	CAGCGTGTAG	GTAATTCCTG	GTATATTTAT	AATAGTAATG	CTAATATCAA	1260
TAAAAATCAG	CAAGTAATGT	TGCCTATGTA	TACTAATAAT	ACAAAGTCGT	TATCGTTAGA	1320
TTTGACGCCA	CATACTTACG	CTGTTGTTAA	AGAAAAATCCA	AATAATTTAC	ATATTTTATT	1380
GAATAATTAC	AGGACAGATA	AGACAGCTAT	GTGGGCATTA	TCAGGAAATT	TTGATGCATC	1440
AAAAAGTTGG	AAGAAAGAAG	AATTAGAGTT	AGCGAACTGG	ATAAGCAAAA	ATTATTCCAT	1500
CAATCCTGTA	GATAATGACT	TTAGGACAAC	AACACTTACA	TTAAAAGGGC	ATACTGGTCA	1560
TAAACCTCAG	ATAAATATAA	GTGGCGATAA	AAATCATTAT	ACTTATACAG	AAAATTGGGA	1620
TGAGAATACC	CATGTTTATA	CCATTACGGT	TAATCATAAT	GGAATGGTAG	AGATGTCTAT	1680
AAATACTGAG	GGGACAGGTC	CAGTCTCTTT	CCCAACACCA	GATAAATTTA	ATGATGGTAA	1740
TTTGAATATA	GCATATGCAA	AACCAACAAC	ACAAAGTTCT	GTAGATTACA	ATGGAGACCC	1800



(2) INFORMATION FOR SEQ ID NO:204:

(A) LENGTH: 657 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys	Ala	Asp	Asn	Arg	Val	Gln	Met	Arg	Thr	Ile	Asn	Asn	Glu	Ser	
1				5					10					15	
Pro	Leu	Leu	Leu	Ser	Pro	Leu	Tyr	Gly	Asn	Asp	Asn	Gly	Asn	Gly	Leu
			20					25					30		
Trp	Trp	Gly	Asn	Thr	Leu	Lys	Gly	Ala	Trp	Glu	Ala	Ile	Pro	Glu	Asp
		35					40					45			
Val	Lys	Pro	Tyr	Ala	Ala	Ile	Glu	Leu	His	Pro	Ala	Lys	Val	Cys	Lys
	50					55					60				
Pro	Thr	Ser	Cys	Ile	Pro	Arg	Asp	Thr	Lys	Glu	Leu	Arg	Glu	Trp	Tyr
65					70					75					80
Val	Lys	Met	Leu	Glu	Glu	Ala	Gln	Ser	Leu	Asn	Ile	Pro	Val	Phe	Leu
				85					90					95	
Val	Ile	Met	Ser	Ala	Gly	Glu	Arg	Asn	Thr	Val	Pro	Pro	Glu	Trp	Leu
			100					105					110		
Asp	Glu	Gln	Phe	Gln	Lys	Tyr	Ser	Val	Leu	Lys	Gly	Val	Leu	Asn	Ile
		115					120					125			
Glu	Asn	Tyr	Trp	Ile	Tyr	Asn	Asn	Gln	Leu	Ala	Pro	His	Ser	Ala	Lys
	130					135					140				
Tyr	Leu	Glu	Val	Cys	Ala	Lys	Tyr	Gly	Ala	His	Phe	Ile	Trp	His	Asp
145					150					155					160
His	Glu	Lys	Trp	Phe	Trp	Glu	Thr	Ile	Met	Asn	Asp	Pro	Thr	Phe	Phe
				165					170					175	
Glu	Ala	Ser	Gln	Lys	Tyr	His	Lys	Asn	Leu	Val	Leu	Ala	Thr	Lys	Asn
			180					185					190		
Thr	Pro	Ile	Arg	Asp	Asp	Ala	Gly	Thr	Asp	Ser	Ile	Val	Ser	Gly	Phe
		195					200					205			
Trp	Leu	Ser	Gly	Leu	Cys	Asp	Asn	Trp	Gly	Ser	Ser	Thr	Asp	Thr	Trp
	210					215					220				
Lys	Trp	Trp	Glu	Lys	His	Tyr	Thr	Asn	Thr	Phe	Glu	Thr	Gly	Arg	Ala

225		230		235		240
Arg Asp Met	Arg Ser Tyr	Ala Ser Glu	Pro Glu Ser	Met Ile Ala	Met	
	245		250		255	
Glu Met Met	Asn Val Tyr	Thr Gly Gly	Gly Thr Val	Tyr Asn Phe	Glu	
	260		265		270	
Cys Ala Ala	Tyr Thr Phe	Met Thr Asn	Asp Val Pro	Thr Pro Ala	Phe	
	275		280		285	
Thr Lys Gly	Ile Ile Pro	Phe Phe Arg	His Ala Ile	Gln Asn Pro	Ala	
	290		295		300	
Pro Ser Lys	Glu Glu Val	Val Asn Arg	Thr Lys Ala	Val Phe Trp	Asn	
305		310		315		320
Gly Glu Gly	Arg Ile Ser	Ser Ser Leu	Asn Gly Phe	Tyr Gln Gly	Leu Tyr	
	325		330		335	
Ser Asn Asp	Glu Thr Met	Pro Leu Tyr	Asn Asn Gly	Arg Tyr His	Ile	
	340		345		350	
Leu Pro Val	Ile His Glu	Lys Ile Asp	Lys Glu Lys	Ile Ser Ser	Ile	
	355		360		365	
Phe Pro Asn	Ala Lys Ile	Leu Thr Lys	Asn Ser Glu	Glu Glu Leu	Ser Ser	
	370		375		380	
Lys Val Asn	Tyr Leu Asn	Ser Leu Tyr	Pro Lys Leu	Tyr Glu Gly	Asp	
385		390		395		400
Gly Tyr Ala	Gln Arg Val	Gly Asn Ser	Trp Tyr Ile	Tyr Asn Ser	Asn	
	405		410		415	
Ala Asn Ile	Asn Lys Asn	Gln Gln Val	Met Leu Pro	Met Tyr Thr	Asn	
	420		425		430	
Asn Thr Lys	Ser Leu Ser	Leu Asp Leu	Thr Pro His	Thr Tyr Ala	Val	
	435		440		445	
Val Lys Glu	Asn Pro Asn	Asn Leu His	Ile Leu Leu	Asn Asn Tyr	Arg	
	450		455		460	
Thr Asp Lys	Thr Ala Met	Trp Ala Leu	Ser Gly Asn	Phe Asp Ala	Ser	
465		470		475		480
Lys Ser Trp	Lys Lys Glu	Glu Glu Leu	Glu Leu Ala	Asn Trp Ile	Ser Lys	
	485		490		495	
Asn Tyr Ser	Ile Asn Pro	Val Asp Asn	Asp Phe Arg	Thr Thr Thr	Leu	
	500		505		510	
Thr Leu Lys	Gly His Thr	Gly His Lys	Pro Gln Ile	Asn Ile Ser	Gly	
	515		520		525	
Asp Lys Asn	His Tyr Thr	Tyr Thr Glu	Asn Trp Asp	Glu Asn Thr	His	
	530		535		540	
Val Tyr Thr	Ile Thr Val	Asn His Asn	Gly Met Val	Glu Met Ser	Ile	
545		550		555		560
Asn Thr Glu	Gly Thr Gly	Pro Val Ser	Phe Pro Thr	Pro Asp Lys	Phe	

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565                      570                      575  
 Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser  
                          580                      585                      590  
 Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg  
                          595                      600                      605  
 Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn  
                          610                      615                      620  
 Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu  
                          625                      630                      635                      640  
 Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn  
                          645                      650                      655  
 Phe

## (2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTC	60
ACGAGAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAA ATCACAGGGA TTCTCAAAAA	120
AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA	180
AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC	240
TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT	300
TTTAGATGGT GAATACCCTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC	360
CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC	420
AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC	480
AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA	540
AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC	600
AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGAATTAAC	660
TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT	720
GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACTTGCAG ACGTTTTTAG	780
TGGCAAATTA ACCACCTGGG ACAAGATTAA A	811

## (2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys	Gly	Asn	Gln	Ser	Ala	Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	1	5	10	15
Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	20	25	30	
Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	35	40	45	
Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	50	55	60	
Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	65	70	75	80
Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	85	90	95	
Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	100	105	110	
Ile	Val	Trp	Ser	Ser	Asn	Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	115	120	125	
Phe	Ile	His	Ser	Lys	Gln	Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	130	135	140	
Ile	Glu	Ala	Lys	Thr	Glu	Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	145	150	155	160
Gly	Lys	Leu	Ser	Val	Val	Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	165	170	175	
Lys	Leu	Ala	Glu	Ala	Tyr	Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	180	185	190	
Ile	Thr	Ser	Asn	Gly	Ser	Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	195	200	205	
Thr	Ala	Asp	Ile	Gly	Met	Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	210	215	220	
Lys	Ser	Leu	Thr	His	Asp	Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	225	230	235	240
Val	Asn	Asn	Asp	Asn	Lys	Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	245	250	255	
Asp	Val	Phe	Ser	Gly	Lys	Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys			260	265	270	

(2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60  
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120  
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTGGAT GCATTTTTTA ATCTCGTTAA 180  
 TGAATAAT ACCATTGTCG GCTCAACTGG CTTATCAGGA GATTTCACCT CCTTTACTCA 240  
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300  
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360  
 GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420  
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480  
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540  
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600  
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTCCTTAT TTGTAGAGAA 660  
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720  
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTTATCAT 780  
 GGATAATGAT AAGTGGGTTA AACTT 805

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser  
 1 5 10 15  
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn  
 20 25 30  
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp  
 35 40 45  
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr  
 50 55 60

Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His  
 65 70 75 80  
 Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys  
 85 90 95  
 Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu  
 100 105 110  
 Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu  
 115 120 125  
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln  
 130 135 140  
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser  
 145 150 155 160  
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser  
 165 170 175  
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His  
 180 185 190  
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu  
 195 200 205  
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu  
 210 215 220  
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys  
 225 230 235 240  
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys  
 245 250 255  
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu  
 260 265

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA 60  
 GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG 120  
 AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT 180  
 CTGGGCTTCT TGGTGTTCCT TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA 240  
 AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTC AAGGACATA AGGGAGAGCA 300  
 ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT 360

AGTTGACCCA TCAGGCAAAC TTTTGGAAAC TTATGGTGTC CGTTCTTACC CAACCCAAGC 420  
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480  
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys	Ser	Gly	Lys	Ser	Val	Thr	Ser	Glu	His	Gln	Thr	Lys	Asp	Glu	Met	1	5	10	15
Lys	Thr	Glu	Gln	Thr	Ala	Ser	Lys	Thr	Ser	Ala	Ala	Lys	Gly	Lys	Glu	20	25	30	
Val	Ala	Asp	Phe	Glu	Leu	Met	Gly	Val	Asp	Gly	Lys	Thr	Tyr	Arg	Leu	35	40	45	
Ser	Asp	Tyr	Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp	50	55	60	
Cys	Ser	Ile	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Thr	Asp	Glu	Ile	Ala	Lys	65	70	75	80
Glu	Ala	Gly	Asp	Asp	Tyr	Val	Val	Leu	Thr	Val	Val	Ser	Pro	Gly	His	85	90	95	
Lys	Gly	Glu	Gln	Ser	Glu	Ala	Asp	Phe	Lys	Asn	Trp	Tyr	Lys	Gly	Leu	100	105	110	
Asp	Tyr	Lys	Asn	Leu	Pro	Val	Leu	Val	Asp	Pro	Ser	Gly	Lys	Leu	Leu	115	120	125	
Glu	Thr	Tyr	Gly	Val	Arg	Ser	Tyr	Pro	Thr	Gln	Ala	Phe	Ile	Asp	Lys	130	135	140	
Glu	Gly	Lys	Leu	Val	Lys	Thr	His	Pro	Gly	Phe	Met	Glu	Lys	Asp	Ala	145	150	155	160
Ile	Leu	Gln	Thr	Leu	Lys	Glu	Leu	Ala	165										

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60  
TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTGTTCT GGGGAGTGGA 120  
GGAATATTTT TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180  
AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240  
CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300  
CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360  
TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420  
GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480  
GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540  
TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600  
GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660  
TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720  
GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTTC 780  
CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840  
TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC 900  
ACAGGACAAG GCGGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA 960  
AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 331 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys  
1 5 10 15  
Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala  
20 25 30  
Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly  
35 40 45  
Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr  
50 55 60  
Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val  
65 70 75 80



(2) INFORMATION FOR SEQ ID NO: 213:

(A) LENGTH: 625 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TTGTCAGTCA GGTTCCTAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA 60  
ATTAGTTGTG GCAACCAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGGTTGATGG 120

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG 180  
 GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAACCTGG 240  
 TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300  
 TTTTTCATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360  
 AAAATACAAG GATTTAAC TA GCCTAGAAAAG TGCTAATATT GCAGCCCAAA AAGGGACTGT 420  
 TCCAGAATCA ATGGTCAAGG AACAATTGCC AAAAGTTCAA TTAACCTCCC TAACTAATAT 480  
 GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTCATA TGGATGAGCC 540  
 TGTTCACCTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600  
 GATGAAGGAC GGCGACGCCA ATGCC 625

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys	Gln	Ser	Gly	Ser	Asn	Gly	Ser	Gln	Ser	Ala	Val	Asp	Ala	Ile	Lys	1	5	10	15
Gln	Lys	Gly	Lys	Leu	Val	Val	Ala	Thr	Ser	Pro	Asp	Tyr	Ala	Pro	Phe	20	25	30	
Glu	Phe	Gln	Ser	Leu	Val	Asp	Gly	Lys	Asn	Gln	Val	Val	Gly	Ala	Asp	35	40	45	
Ile	Asp	Met	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Gly	Val	Lys	Leu	Glu	50	55	60	
Ile	Ser	Ser	Met	Ser	Phe	Asp	Asn	Val	Leu	Thr	Ser	Leu	Gln	Thr	Gly	65	70	75	80
Lys	Ala	Asp	Leu	Ala	Val	Ala	Gly	Ile	Ser	Ala	Thr	Asp	Glu	Arg	Lys	85	90	95	
Glu	Val	Phe	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Glu	Asn	Lys	Ile	Ser	Phe	100	105	110	
Leu	Val	Arg	Lys	Ala	Asp	Val	Glu	Lys	Tyr	Lys	Asp	Leu	Thr	Ser	Leu	115	120	125	
Glu	Ser	Ala	Asn	Ile	Ala	Ala	Gln	Lys	Gly	Thr	Val	Pro	Glu	Ser	Met	130	135	140	
Val	Lys	Glu	Gln	Leu	Pro	Lys	Val	Gln	Leu	Thr	Ser	Leu	Thr	Asn	Met	145	150	155	160
Gly	Glu	Ala	Val	Asn	Glu	Leu	Gln	Ala	Gly	Lys	Ile	Asp	Ala	Val	His				

0076527103001  
 T2559260

165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu  
 180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATT GTGAATAAAA ACACAGAAAA	180
TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAAC TAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA	600
CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTC	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT	900
CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTG TAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC	1020
TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GCTCCTAGTA AATTAAATTT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380  
 TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA 1440  
 TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500  
 GGATGAAGGT ACTAAAAGTC AAGTGTTTTT AATTTTCAGGA GATGATGGTG TAAAGCTATG 1560  
 GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620  
 AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA 1680  
 TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA 1740  
 TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800  
 TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860  
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920  
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980  
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040  
 TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100  
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160  
 AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAAACTCA TATGGTTCCA TTTCTCTTAA 2220  
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280  
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340  
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT 2400  
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460  
 CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520  
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGA GCGATGGAAG CTCTAAACTC 2580  
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG 2640  
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700  
 AACACTGGGA GGTATATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760  
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820  
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880  
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940  
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAG 3000  
 AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

00765274.012004

- (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Thr	Ala	Val	Ile	Lys	Glu	1	5	10	15
Lys	Glu	Val	Val	Ser	Lys	Asn	Pro	Val	Ile	Asp	Asn	Asn	Thr	Ser	Asn	20	25	30	
Glu	Glu	Ala	Lys	Ile	Lys	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp	35	40	45	
Tyr	Thr	Asp	Ser	Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu	50	55	60	
Asp	Lys	Val	Val	Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu	65	70	75	80
Lys	Ala	Ile	Lys	Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr	85	90	95	
Thr	Tyr	Asp	Arg	Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Thr	Pro	Asp	100	105	110	
Asn	Leu	Asp	Lys	Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg	115	120	125	
Ala	Gln	Lys	Val	Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly	130	135	140	
Val	Glu	Glu	Ala	Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly	145	150	155	160
Lys	Asn	Phe	Asp	Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly	165	170	175	
Thr	Asp	Tyr	Arg	His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala	180	185	190	
Ser	Met	Arg	Phe	Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Tyr	195	200	205	
Trp	Leu	Ser	Asp	Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly	210	215	220	
Lys	Ile	Thr	Val	Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro	225	230	235	240
His	Gly	Met	His	Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln	245	250	255	
Asp	Ile	Lys	Asn	Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln	260	265	270	
Ile	Phe	Ser	Tyr	Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly	275	280	285	

Asp	Glu	Thr	Met	Phe	His	Ala	Ile	Glu	Asp	Ser	Ile	Lys	His	Asn	Val
290						295					300				
Asp	Val	Val	Ser	Val	Ser	Ser	Gly	Phe	Thr	Gly	Thr	Gly	Leu	Val	Gly
305					310					315					320
Glu	Lys	Tyr	Trp	Gln	Ala	Ile	Arg	Ala	Leu	Arg	Lys	Ala	Gly	Ile	Pro
				325					330					335	
Met	Val	Val	Ala	Thr	Gly	Asn	Tyr	Ala	Thr	Ser	Ala	Ser	Ser	Ser	Ser
			340					345					350		
Trp	Asp	Leu	Val	Ala	Asn	Asn	His	Leu	Lys	Met	Thr	Asp	Thr	Gly	Asn
		355					360					365			
Val	Thr	Arg	Thr	Ala	Ala	His	Glu	Asp	Ala	Ile	Ala	Val	Ala	Ser	Ala
	370					375					380				
Lys	Asn	Gln	Thr	Val	Glu	Phe	Asp	Lys	Val	Asn	Ile	Gly	Gly	Glu	Ser
385					390					395					400
Phe	Lys	Tyr	Arg	Asn	Ile	Gly	Ala	Phe	Phe	Asp	Lys	Ser	Lys	Ile	Thr
				405					410					415	
Thr	Asn	Glu	Asp	Gly	Thr	Lys	Ala	Pro	Ser	Lys	Leu	Lys	Phe	Val	Tyr
			420					425					430		
Ile	Gly	Lys	Gly	Gln	Asp	Gln	Asp	Leu	Ile	Gly	Leu	Asp	Leu	Arg	Gly
		435					440					445			
Lys	Ile	Ala	Val	Met	Asp	Arg	Ile	Tyr	Thr	Lys	Asp	Leu	Lys	Asn	Ala
	450					455					460				
Phe	Lys	Lys	Ala	Met	Asp	Lys	Gly	Ala	Arg	Ala	Ile	Met	Val	Val	Asn
465					470					475					480
Thr	Val	Asn	Tyr	Tyr	Asn	Arg	Asp	Asn	Trp	Thr	Glu	Leu	Pro	Ala	Met
				485					490					495	
Gly	Tyr	Glu	Ala	Asp	Glu	Gly	Thr	Lys	Ser	Gln	Val	Phe	Ser	Ile	Ser
			500					505					510		
Gly	Asp	Asp	Gly	Val	Lys	Leu	Trp	Asn	Met	Ile	Asn	Pro	Asp	Lys	Lys
		515					520					525			
Thr	Glu	Val	Lys	Arg	Asn	Asn	Lys	Glu	Asp	Phe	Lys	Asp	Lys	Leu	Glu
	530					535					540				
Gln	Tyr	Tyr	Pro	Ile	Asp	Met	Glu	Ser	Phe	Asn	Ser	Asn	Lys	Pro	Asn
545					550					555					560
Val	Gly	Asp	Glu	Lys	Glu	Ile	Asp	Phe	Lys	Phe	Ala	Pro	Asp	Thr	Asp
				565					570					575	
Lys	Glu	Leu	Tyr	Lys	Glu	Asp	Ile	Ile	Val	Pro	Ala	Gly	Ser	Thr	Ser
			580					585					590		
Trp	Gly	Pro	Arg	Ile	Asp	Leu	Leu	Leu	Lys	Pro	Asp	Val	Ser	Ala	Pro
		595					600					605			
Gly	Lys	Asn	Ile	Lys	Ser	Thr	Leu	Asn	Val	Ile	Asn	Gly	Lys	Ser	Thr
	610					615					620				

Tyr 625	Gly	Tyr	Met	Ser	Gly 630	Thr	Ser	Met	Ala	Thr 635	Pro	Ile	Val	Ala	Ala 640
Ser	Thr	Val	Leu	Ile 645	Arg	Pro	Lys	Leu	Lys 650	Glu	Met	Leu	Glu	Arg 655	Pro
Val	Leu	Lys	Asn 660	Leu	Lys	Gly	Asp	Asp 665	Lys	Ile	Asp	Leu	Thr 670	Ser	Leu
Thr	Lys	Ile 675	Ala	Leu	Gln	Asn	Thr 680	Ala	Arg	Pro	Met	Met 685	Asp	Ala	Thr
Ser	Trp 690	Lys	Glu	Lys	Ser	Gln 695	Tyr	Phe	Ala	Ser	Pro 700	Arg	Gln	Gln	Gly
Ala 705	Gly	Leu	Ile	Asn 710	Val	Ala	Asn	Ala	Leu	Arg 715	Asn	Glu	Val	Val	Ala 720
Thr	Phe	Lys	Asn 725	Thr	Asp	Ser	Lys	Gly	Leu 730	Val	Asn	Ser	Tyr	Gly 735	Ser
Ile	Ser	Leu	Lys 740	Glu	Ile	Lys	Gly	Asp 745	Lys	Lys	Tyr	Phe	Thr 750	Ile	Lys
Leu	His 755	Asn	Thr	Ser	Asn	Arg	Pro 760	Leu	Thr	Phe	Lys	Val 765	Ser	Ala	Ser
Ala 770	Ile	Thr	Thr	Asp	Ser	Leu 775	Thr	Asp	Arg	Leu	Lys 780	Leu	Asp	Glu	Thr
Tyr 785	Lys	Asp	Glu	Lys	Ser 790	Pro	Asp	Gly	Lys	Gln 795	Ile	Val	Pro	Glu	Ile 800
His	Pro	Glu	Lys 805	Val	Lys	Gly	Ala	Asn 810	Ile	Thr	Phe	Glu	His 815	Asp	Thr
Phe	Thr	Ile 820	Gly	Ala	Asn	Ser	Ser	Phe 825	Asp	Leu	Asn	Ala 830	Val	Ile	Asn
Val	Gly 835	Glu	Ala	Lys	Asn	Lys	Asn 840	Lys	Phe	Val	Glu	Ser 845	Phe	Ile	His
Phe 850	Glu	Ser	Val	Glu	Ala	Met 855	Glu	Ala	Leu	Asn	Ser 860	Ser	Gly	Lys	Lys
Ile 865	Asn	Phe	Gln	Pro	Ser 870	Leu	Ser	Met	Pro	Leu 875	Met	Gly	Phe	Ala	Gly 880
Asn	Trp	Asn	His 885	Glu	Pro	Ile	Leu	Asp	Lys 890	Trp	Ala	Trp	Glu	Glu 895	Gly
Ser	Arg	Ser	Lys 900	Thr	Leu	Gly	Gly	Tyr 905	Asp	Asp	Asp	Gly	Lys 910	Pro	Lys
Ile 915	Pro	Gly	Thr	Leu	Asn	Lys	Gly 920	Ile	Gly	Gly	Glu	His 925	Gly	Ile	Asp
Lys 930	Phe	Asn	Pro	Ala	Gly	Val 935	Ile	Gln	Asn	Arg	Lys 940	Asp	Lys	Asn	Thr
Thr 945	Ser	Leu	Asp	Gln	Asn 950	Pro	Glu	Leu	Phe	Ala 955	Phe	Asn	Asn	Glu	Gly 960

Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro  
 965 970 975

Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu  
 980 985 990

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile  
 995 1000 1005

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA	60
CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAAACAG AAGAAAGTCC	120
AAAGGAAGAA CCAAATCGG AGGTAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA	180
GGGGAAGAA GATTGAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC	240
AAAACCAGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA	300
GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC	360
AGTCGAGCCA GAAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAAACACC	420
GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA	480
GACTGTTAAT CAATCTATTG AACAACCAA AGTTGAAACG CCTGCTGTAG AAAACAAAC	540
AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA	600
CGAAGAGGCA CCAACGGCAC CAGTTGAGCC AGAAAAGCAA CCAGAAGTTC CTGAAGAAGA	660
GAAGGCTGTA GAGGAAACAC CGAAACCAGA AGATAAAATA AAGGGTATTG GTACTAAAGA	720
ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTTCTCCTAC	780
TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAAACTG CAAAAGGTGT	840
CTATGCTTCA GAGCCTGTAA AACAGCCTGA GGTAAATAGC GAGACAAATA AACTTAAAC	900
GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA	960
AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC	1020
AAAGGCTGAA AAAGTTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT	1080
TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTGAATTA TCTGAAAAGC CAATATTAAC	1140
ATTGACTAGT ACCGATAAGA AAATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA	1200
AAATCAAAAC AAAACAAAA TCAAATCAAT CACAGCTGAA TTGAAAAAG GAGAAGAAGT	1260



TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAAACTATAA GCGCTGCATT 1320  
 TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG 1380  
 TAACGGTGAA GAAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAAGT 1440  
 TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAAACTAA 1500  
 TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTTAA AAATAACTTC 1560  
 AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTAACGG 1620  
 AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680  
 TAAATTTGAA GAAGAA 1696

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val	Val	Glu	Val	Glu	Thr	Pro	Gln	Ser	Ile	Thr	Asn	Gln	Glu	Gln	Ala	1	5	10	15
Arg	Thr	Glu	Asn	Gln	Val	Val	Glu	Thr	Glu	Glu	Ala	Pro	Lys	Glu	Glu	20	25	30	
Ala	Pro	Lys	Thr	Glu	Glu	Ser	Pro	Lys	Glu	Glu	Pro	Lys	Ser	Glu	Val	35	40	45	
Lys	Pro	Thr	Asp	Asp	Thr	Leu	Pro	Lys	Val	Glu	Glu	Gly	Lys	Glu	Asp	50	55	60	
Ser	Ala	Glu	Pro	Ala	Pro	Val	Glu	Glu	Val	Gly	Gly	Glu	Val	Glu	Ser	65	70	75	80
Lys	Pro	Glu	Glu	Lys	Val	Ala	Val	Lys	Pro	Glu	Ser	Gln	Pro	Ser	Asp	85	90	95	
Lys	Pro	Ala	Glu	Glu	Ser	Lys	Val	Glu	Gln	Ala	Gly	Glu	Pro	Val	Ala	100	105	110	
Pro	Arg	Glu	Asp	Glu	Lys	Ala	Pro	Val	Glu	Pro	Glu	Lys	Gln	Pro	Glu	115	120	125	
Ala	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	Gln	Glu	Glu	130	135	140	
Ser	Thr	Pro	Asp	Thr	Lys	Ala	Glu	Glu	Thr	Val	Glu	Pro	Lys	Glu	Glu	145	150	155	160
Thr	Val	Asn	Gln	Ser	Ile	Glu	Gln	Pro	Lys	Val	Glu	Thr	Pro	Ala	Val	165	170	175	
Glu	Lys	Gln	Thr	Glu	Pro	Thr	Glu	Glu	Pro	Lys	Val	Glu	Gln	Ala	Gly				

180					185					190				
Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro
		195					200					205		Val
Glu	Pro	Glu	Lys	Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val
		210					215					220		Glu
Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys
							230					235		240
Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser
				245					250					255
Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	Ala	Ser	Tyr	Asn	Ala	Leu	Gly
				260					265					270
Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	Tyr	Ala	Ser	Glu	Pro	Val	Lys
							280					285		Gln
Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	Lys	Leu	Lys	Thr	Ala	Ile	Asp
							295					300		Ala
Leu	Asn	Val	Asp	Lys	Thr	Glu	Leu	Asn	Asn	Thr	Ile	Ala	Asp	Lys
												315		320
Thr	Lys	Val	Lys	Glu	His	Tyr	Ser	Asp	Arg	Ser	Trp	Gln	Asn	Gln
									330					335
Thr	Glu	Val	Thr	Lys	Ala	Glu	Lys	Val	Ala	Ala	Asn	Thr	Asp	Lys
									345					350
Gln	Ser	Glu	Val	Asn	Glu	Ala	Val	Glu	Lys	Leu	Thr	Ala	Thr	Ile
							360					365		Glu
Lys	Leu	Val	Glu	Leu	Ser	Glu	Lys	Pro	Ile	Leu	Thr	Leu	Thr	Ser
							375					380		Thr
Asp	Lys	Lys	Ile	Leu	Glu	Arg	Glu	Ala	Val	Ala	Lys	Tyr	Thr	Glu
												395		400
Asn	Gln	Asn	Lys	Thr	Lys	Ile	Lys	Ser	Ile	Thr	Ala	Glu	Leu	Lys
									410					415
Gly	Glu	Glu	Val	Ile	Asn	Thr	Val	Val	Leu	Thr	Asp	Asp	Lys	Val
									425					430
Thr	Glu	Thr	Ile	Ser	Ala	Ala	Phe	Lys	Asn	Leu	Glu	Tyr	Tyr	Lys
									440					445
Tyr	Thr	Leu	Ser	Thr	Thr	Met	Ile	Tyr	Asp	Arg	Gly	Asn	Gly	Glu
												460		Glu
Thr	Glu	Thr	Leu	Glu	Asn	Gln	Asn	Ile	Gln	Leu	Asp	Leu	Lys	Lys
														480
Glu	Leu	Lys	Asn	Ile	Lys	Arg	Thr	Asp	Leu	Ile	Lys	Tyr	Glu	Asn
									490					495
Lys	Glu	Thr	Asn	Glu	Ser	Leu	Ile	Thr	Thr	Ile	Pro	Asp	Asp	Lys
									505					510
Asn	Tyr	Tyr	Leu	Lys	Ile	Thr	Ser	Asn	Asn	Gln	Lys	Thr	Thr	Leu
														Leu

515	520	525
Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn Gly Thr Pro Val Tyr		
530	535	540
Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg Thr Ala Asp Asn		
545	550	555 560
Lys Phe Glu Glu Glu		
565		

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA	60
TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT	120
ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAAC GATCCTTCAA AAGAATATCG	180
TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA	240
AGAATTCACA GGAAACTTTT TAAGTTCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA	300
ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT	360
AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATTG GCCAATACTA TGAAAGGTTC	420
TTCAAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTCGTAATA ATGTTGCTGG	480
ATTTGTAAAT AATATGAATG ATGGAACCTG TATTGAAAAT GTTGCTTTCT TTGGCAAACCT	540
ACACTCTACA AGTGGAATG GCTCTCATAC AGGGGGAATT GCAGGTACAA ACTATAGAGG	600
AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT	660
GTTAGTTCCT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT	720
CCTAACTGAG TCGGTTGTAA AAGGTAAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC	780
AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT	840
TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC	900
TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCGTCA GGTAATAGAT CATTTAGGAA	960
ATCTAAACA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA	1020
TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAAACTTA ATGAAGAAAA	1080
AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA	1140
AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA	1200

AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260  
TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320  
TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380  
TGACTIONAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440  
TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500  
AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560  
CACAGATGTT AAAGAAAACCT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620  
TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680  
AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740  
TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800  
ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860  
CGACGCATTC GGTCAAGTA 1879

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile	Ala	Asp	Asn	Leu	Val	Ser	Arg
1				5					10					15	
Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu	Tyr	Val	His	Tyr	Ile	Glu	Lys
			20					25					30		
Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr	Tyr	Asn	Phe	Lys	Glu	Leu	Val
		35					40					45			
Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys	Glu	Tyr	Arg	Leu	Gly	Gln	Ser
		50				55					60				
Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn	Gly	Lys	Ser	Tyr	Ile	Thr	Lys
				70					75					80	
Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser	Glu	Gly	Lys	Gln	Phe	Ala	Ile
			85					90					95		
Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn	Val	Ile	Thr	Asn	Ala	Thr	Ile
			100					105					110		
Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu	Ile	Glu	Arg	Ser	Gly	Gln	Asp
		115					120					125			
Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met	Lys	Gly	Ser	Ser	Val	Ile	Thr
		130					135					140			

Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly  
 145 150 155 160  
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe  
 165 170 175  
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly  
 180 185 190  
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp  
 195 200 205  
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys  
 210 215 220  
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu  
 225 230 235 240  
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val  
 245 250 255  
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser  
 260 265 270  
 Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly  
 275 280 285  
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp  
 290 295 300  
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys  
 305 310 315 320  
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val  
 325 330 335  
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro  
 340 345 350  
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr  
 355 360 365  
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro  
 370 375 380  
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys  
 385 390 395 400  
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn  
 405 410 415  
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val  
 420 425 430  
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser Ser  
 435 440 445  
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile  
 450 455 460  
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn  
 465 470 475 480

0076527 0400  
 T0220 T255260

Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met  
 485 490 495  
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys  
 500 505 510  
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr  
 515 520 525  
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp  
 530 535 540  
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys  
 545 550 555 560  
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val  
 565 570 575  
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp  
 580 585 590  
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly  
 595 600 605  
 Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly  
 610 615 620  
 Gln Val  
 625

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TAAAAAATTC	240
TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCCTTGG	360
TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420
TGCAGATGGT TATAGAAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTTAA	480
ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTATAACG CTCCTGGTGG	540
ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT	600

(2) INFORMATION FOR SEQ ID NO:222:

(A) LENGTH: 592 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His

50

55

60

Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser		
65	70	75 80
Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr		
	85	90 95
Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser		
	100	105 110
Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys		
	115	120 125
Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr		
	130	135 140
Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys		
	145	150 155 160
Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn		
	165	170 175
Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys		
	180	185 190
Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr		
	195	200 205
Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp		
	210	215 220
Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu		
	225	230 235 240
Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg		
	245	250 255
Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu		
	260	265 270
Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe		
	275	280 285
Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn		
	290	295 300
Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg		
	305	310 315 320
Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu		
	325	330 335
Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp		
	340	345 350
Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn		
	355	360 365
Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu		
	370	375 380
Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln		

09765374-043304



(2) INFORMATION FOR SEQ ID NO: 223:

(A) LENGTH: 460 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TAAGACAGAT	GAACGGAGCA	AGGTGTTTGA	CTTTTCCATT	CCCTACTATA	CTGCAAAAAA	60
TAAACTCATT	GTCAAAAAAT	CTGACTTGAC	TACTTATCAG	TCTGTAAACG	ACTTGCGCGCA	120
GAAAAAGGTT	GGAGCGCAGA	AAGGTTTCGAT	TCAAGAGACG	ATGGCGAAAG	ATTTGCTACA	180
AAATTCTTCC	CTCGTATCTC	TGCCTAAAAA	TGGGAATTTA	ATCACAGATT	TAAAATCAGG	240
ACAAGTGGAT	GCCGTTATCT	TTGAAGAACC	TGTTTCCAAG	GGATTGTGG	AAAATAATCC	300
TGATTTAGCA	ATCGCAGACC	TCAATTTTGA	AAAAGAGCAA	GATGATTCCT	ACGCGGTAGC	360
CATgAAAAAA	GATAGCAAGA	AATTGAAGAG	GCAGTTCGAT	AAAACCATT	AAAAGTTGAA	420

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
1          5          10          15
Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
20          25          30
Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
35          40          45
Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
50          55          60
Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
65          70          75          80
Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
85          90          95
Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
100         105         110
Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
115         120         125
Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
130         135         140
Leu Asp Lys Leu Ile Glu Glu Ala Leu
145         150

```

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC      60
AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT      120
CGAAGTTTTA AAGGCAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC      180

```

CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240  
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300  
 TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360  
 TAAAACAACA CAAGAGGATA CCGGAACCTC TAACGCTCAA TTCATCAATA ACTGGAATCA 420  
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480  
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540  
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600  
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660  
 GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAAACTC AGCAATACCT ATCTAGGTGG 720  
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile  
 1 5 10 15  
 Val Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys  
 20 25 30  
 Gly Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu  
 35 40 45  
 Lys Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser  
 50 55 60  
 Ile Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn  
 65 70 75 80  
 Leu Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro  
 85 90 95  
 Ile Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu  
 100 105 110  
 Thr Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly  
 115 120 125  
 Thr Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp  
 130 135 140  
 Asn Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile  
 145 150 155 160

00765271-012201

(2) INFORMATION FOR SEQ ID NO: 227:

(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 33

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 27

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 30

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTGAC TAACCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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32

32

(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

45

(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

33

33

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

35

(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

32

32

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAATAT GGTAAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

37

37

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37

37

(2) INFORMATION FOR SEQ ID NO: 248:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTTGTTT GCTTGGTATT GGTCG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

36

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31

- 38

37

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCAGTGCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

34

36

37

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37

(2) INFORMATION FOR SEQ ID NO: 284:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

30

37

36

35

(2) INFORMATION FOR SEQ ID NO: 293:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTTCTG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

0076924-013904

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTAA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

36

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

43

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

34

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

38

(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

37

(2) INFORMATION FOR SEQ ID NO: 311:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

0076527 042004



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGTCGAC ATTAGGAGCC ACTGGTCTC

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

32

33

30

28

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0976327 04300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

00765974 0133001

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

35

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

36

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

34

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

37

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

(2) INFORMATION FOR SEO ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0076527 042204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTTGATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

00765274 013001



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGGAAGGG

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGGATCC TCAAAAAGAG AAGGAAAAC TGG

33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGTACCAG-CAACAAAGCG AGCAAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

40.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTTGTCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765974-012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

(2) INFORMATION FOR SEQ ID NO: 365:

0075541000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

00765274 0122004

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG

47

(2) INFORMATION FOR SEQ ID NO: 392:

0076527 012204



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

37

36

34

35

31

31

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

00763274 043204

GACTGGATCC GTGGATGGGC TTTAACTATC TTCGTATTCG

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGTCAAGCTT GCTAGTCTTC ACTTTCCCTT TCC

33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

### 3.4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

'CAGTGGATCC—TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTSTAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

34

—

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

38

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

33

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

30

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

36

(2) INFORMATION FOR SEQ ID NO: 419:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTGAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTTT CAATATTTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTC AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTCAAGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

39

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

32'

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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